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May 25, 2000

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 Washington, DC 20231

Presented for filing is a new continuation-in-part patent application of:

APPLICANTS: JAY M. SHORT AND KEITH A. KRETZ  
 TITLE: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF

Enclosed are the following papers, including all those required for a filing date under 37 CFR § 1.53(b):

|                                    |                               |
|------------------------------------|-------------------------------|
| Pages of Specification             | 122                           |
| Pages of Claims                    | 6                             |
| Pages of Abstract                  | 1                             |
| Pages of Declaration               | 3 (unsigned)                  |
| Sheets of Drawing                  | 3                             |
| Pages of Small Entity Statement    | [to be filed at a later date] |
| Permission to Use Sequence Listing | 2                             |
| Pages of Sequence                  | 5                             |

Under 35 USC § 120, this application claims the benefit of prior US application 09/318,528, filed May 25, 1999, which is a continuation-in-part of U.S. Patent Application Serial No. 09/291,931, filed April 13, 1999, which is a continuation-in-part of U.S. Patent Application Serial No. 09/259,214, filed March 1, 1999, which is a divisional of U.S. Patent Application Serial No. 08/910,798, now U.S. Patent No. 5,876,997, filed August 13, 1997.

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| <p>"EXPRESS MAIL" Mailing Label Number <b>EL476993090US</b><br/>                     Date of Deposit <b>May 25, 2000</b><br/>                     I hereby certify under 37 CFR § 1.10 that this correspondence is being deposited with the United States Postal Service as "Express Mail Post Office To Addressee" with sufficient postage on the date indicated above and is addressed to the Assistant Commissioner for Patents, Washington, DC 20231. <b>Mikhail Bayley</b><br/> <i>Mikhail Bayley</i></p> |
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**Gray Cary Ware & Freidenrich LLP**

DOCKET NO. DIVER1370-4

In Re Application of: Short et al.

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| Basic filing fee                                 | \$ | 0.00 |
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Please defer the payment of the filing fee until the filing of the Declaration. Please charge any other required fees, **EXCEPT FOR THE FILING FEE**, or credit any overpayments, to Deposit Account 50-1355, referencing the Attorney Docket number shown above. A copy of this transmittal letter is attached.

If this application is found to be INCOMPLETE, or if it appears that a telephone conference would helpfully advance prosecution, please telephone the undersigned at (858) 677-1456.

Kindly acknowledge receipt of this application by returning the enclosed postcard.

Respectfully submitted,



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5/25/00  
Date

**Enclosures**

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**RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF****CROSS-REFERENCE TO RELATED APPLICATIONS**

This application is a continuation-in-part of U.S. Patent Application 09/318,528,  
5 filed May 25, 1999, which is a continuation-in-part of U.S. Patent Application Serial  
No. 09/291,931, filed April 13, 1999, which is a continuation of U.S. Patent  
Application Serial No. 09/259,214, filed March 1, 1999, which is a divisional of U.S.  
Patent Application Serial No. 08/910,798, now U.S. Patent No. 5,876,997, filed August  
13, 1997, all of which are hereby incorporated by reference in their entirety.

**1. FIELD OF THE INVENTION**

This invention relates to newly identified polynucleotides, polypeptides encoded  
by such polynucleotides, the use of such polynucleotides and polypeptides, as well as  
the production and isolation of such polynucleotides and polypeptides. More  
15 particularly, the polypeptides of the present invention have been identified as phytases  
and in particular, microbial enzymes having phytase activity.

**2. BACKGROUND**

**2.1.1 - Brief Summary:** Minerals are essential elements for the growth of all  
organisms. Dietary minerals can be derived from many source materials, including  
plants. *E.g.*, plant seeds are a rich source of minerals since they contain ions that are  
complexed with the phosphate groups of phytic acid molecules. These phytate-  
associated minerals satisfy the dietary needs of some species of farmed organisms, such  
20 as multi-stomached ruminants. Accordingly, ruminants do not require dietary  
supplementation with inorganic phosphate and minerals because microorganisms in the  
rumen produce enzymes that catalyze conversion of phytate (myo-inositol-  
hexaphosphate) to inositol and inorganic phosphate. In the process, minerals that have  
been complexed with phytate are released. The majority of species of farmed  
30 organisms, however, are unable to efficiently utilize phytate-associated minerals. Thus,  
for example, in the livestock production of monogastric animals (*e.g.*, pigs, birds, and  
fish), feed is commonly supplemented with minerals &/or with antibiotic substances

that alter the digestive flora environment of the consuming organism to enhance growth rates.

As such, there are many problematic burdens - related to nutrition, ex vivo processing steps, health and medicine, environmental conservation, and resource management – that are associated with an insufficient hydrolysis of phytate in many applications. The following are non-limiting examples of these problems:

- 1) The supplementation of diets with inorganic minerals is a costly expense.
- 2) The presence of unhydrolyzed phytate is undesirable and problematic in many ex vivo applications (*e.g.* by causing the presence of unwanted sludge).
- 3) The supplementation of diets with antibiotics poses a medical threat to humans and animals alike by increasing the abundance of antibiotic-tolerant pathogens.
- 4) The discharge of unabsorbed fecal minerals into the environment disrupts and damages the ecosystems of surrounding soils, fish farm waters, and surface waters at large.
- 5) The valuable nutritional offerings of many potential foodstuffs remain significantly untapped and squandered.

**2.1.2 - Nutritional Concerns:** Many potentially nutritious plants, including particularly their seeds, contain appreciable amounts of nutrients, *e.g.* phosphate, that are associated with phytate in a manner such that these nutrients are not freely available upon consumption. The unavailability of these nutrients is overcome by some organisms, including cows and other ruminants, that have a sufficient digestive ability - largely derived from the presence of symbiotic life forms in their digestive tracts – to hydrolyze phytate and liberate the associated nutrients. However, the majority of species of farmed animals, including pigs, fish, chickens, turkeys, as well as other non-ruminant organisms including man, are unable to efficiently liberate these nutrients after ingestion.

Consequently, phytate-containing foodstuffs require supplementation with exogenous nutrients and/or with a source of phytase activity in order to amend their

deficient nutritional offerings upon consumption by a very large number of species of organisms.

**2.1.3 - Ex vivo Processing Concerns:** In yet another aspect, the presence of unhydrolyzed phytate leads to problematic consequences in ex vivo processes including - but not limited to - the processing of foodstuffs. In but merely one exemplification, as described in EP0321004-B1 (Vaara *et al.*), there is a step in the processing of corn and sorghum kernels whereby the hard kernels are steeped in water to soften them. Water-soluble substances that leach out during this process become part of a corn steep liquor, which is concentrated by evaporation. Unhydrolyzed phytic acid in the corn steep liquor, largely in the form of calcium and magnesium salts, is associated with phosphorus and deposits an undesirable sludge with proteins and metal ions. This sludge is problematic in the evaporation, transportation and storage of the corn steep liquor. Accordingly, the instantly disclosed phytase molecules - either alone or in combination with other reagents (including but not limited to enzymes, including proteases) - are serviceable not only in this application (*e.g.*, for prevention of the unwanted slugde) but also in other applications where phytate hydrolysis is desirable.

**2.1.4 - Medical Concerns:** The supplementation of diets with antibiotic substances has many beneficial results in livestock production. For example, in addition to its role as a prophylactic means to ward off disease, the administration of exogenous antibiotics has been shown to increase growth rates by upwards of 3-5%. The mechanism of this action may also involve – in part – an alteration in the digestive flora environment of farmed animals, resulting in a microfloral balance that is more optimal for nutrient absorption.

However, a significant negative effect associated with the overuse of antibiotics is the danger of creating a repository of pathogenic antibiotic-resistant microbial strains. This danger is imminent, and the rise of drug-resistant pathogens in humans has already been linked to the use of antibiotics in livestock. For example, Avoparcin, the antibiotic used in animal feeds, was banned in many places in 1997, and animals are now being given another antibiotic, virginiamycin, which is very similar to the new drug, Synercid, used to replace vancomycin in human beings. However, studies have

already shown that some enterococci in farm animals are resistant to Synercid.

Consequently, undesired tolerance consequences, such as those already seen with Avoparcin and vancomycin, are likely to reoccur no matter what new antibiotics are used as blanket prophylactics for farmed animals. Accordingly, researchers are calling  
5 for tighter controls on drug use in the industry.

The increases in growth rates achieved in animals raised on foodstuffs supplemented with the instantly disclosed phytase molecules matches – if not exceeds – those achieved using antibiotics such as, for example, Avoparcin. Accordingly, the  
10 instantly disclosed phytase molecules - either alone or in combination with other reagents (including but not limited to enzymes, including proteases) - are serviceable not only in this application (*e.g.*, for increasing the growth rate of farmed animals) but also in other applications where phytate hydrolysis is desirable.

**2.1.5 - Environmental Concerns:** An environmental consequence is that the consumption of phytate-containing foodstuffs by any organism species that is phytase-deficient - regardless of whether the foodstuffs are supplemented with minerals - leads to fecal pollution resulting from the excretion of unabsorbed minerals. This pollution has a negative impact not only on the immediate habitat but consequently also on the  
20 surrounding waters. The environmental alterations occur primarily at the bottom of the food chain, and therefore have the potential to permeate upwards and throughout an ecosystem to effect permanent and catastrophic damage – particularly after years of continual pollution. This problem has the potential to manifest itself in any area where concentrated phytate processing occurs – including *in vivo* (*e.g.* by animals in areas of  
25 livestock production, zoological grounds, wildlife refuges, etc.) and *in vitro* (*e.g.* in commercial corn wet milling, cereal steeping processes, etc.) processing steps.

**2.1.6 - Financial Concerns:** The decision to use exogenously added phytase molecules – whether to fully replace or to augment the use of exogenously administered  
30 minerals &/or antibiotics – ultimately needs to pass a test of financial feasibility & cost effectiveness by the user whose livelihood depends on the relevant application, such as livestock production.

Consequently, there is a need for means to achieve efficient and cost effective hydrolysis of phytate in various applications. Particularly, there is a need for means to optimize the hydrolysis of phytate in commercial applications. In a particular aspect, there is a need to optimize commercial treatment methods that improve the nutritional offerings of phytate-containing foodstuffs for consumption by humans and farmed animals.

Previous reports of recombinant phytases are available, but their inferior activities are eclipsed by the newly discovered phytase molecules of instant invention. Accordingly, the instantly disclosed phytase molecules are counted upon to provide substantially superior commercial performance than previously identified phytase molecules, *e.g.* phytase molecules of fungal origin.

## 2.2 - General Overview of Phytate & Phytate Hydrolysis

**2.2.1 - Phytate Hydrolysis Leads to Release of Nutrients:** Phytate occurs as a source of stored phosphorous in virtually all plant feeds (Graf (Ed.), 1986). Phytic acid forms a normal part of the seed in cereals and legumes. It functions to bind dietary minerals that are essential to the new plant as it emerges from the seed. When the phosphate groups of phytic acid are removed by the seed enzyme phytase, the ability to bind metal ions is lost and the minerals become available to the plant. In livestock feed grains, the trace minerals bound by phytic acid are largely unavailable for absorption by monogastric animals, which lack phytase activity.

Although some hydrolysis of phytate occurs in the colon, most phytate passes through the gastrointestinal tract of monogastric animals and is excreted in the manure contributing to fecal phosphate pollution problems in areas of intense livestock production. Inorganic phosphorous released in the colon has an appreciably diminished nutritional value to livestock because inorganic phosphorous is absorbed mostly – if not virtually exclusively - in the small intestine. Thus, an appreciable amount of the nutritionally important dietary minerals in phytate is unavailable to monogastric animals.



In sum, phytate-associated nutrients are comprised of not only phosphate that is covalently linked to phytate, but also other minerals that are chelated by phytate as well. Moreover, upon injection, unhydrolyzed phytate may further encounter and become associated with additional minerals. The chelation of minerals may inhibit the activity of enzymes for which these minerals serve as co-factors.

**2.2.2 - Microbial Enzymes Can Hydrolyze Phytate:** Conversion of phytate to inositol and inorganic phosphorous can be catalyzed by microbial enzymes referred to broadly as phytases. Phytases such as phytase #EC 3.1.3.8 are capable of catalyzing the hydrolysis of myo-inositol hexaphosphate to D-myo-inositol 1,2,4,5,6-pentaphosphate and orthophosphate. Certain fungal phytases reportedly hydrolyze inositol pentaphosphate to tetra-, tri-, and lower phosphates. *E.g.*, *A. ficuum* phytases reportedly produce mixtures of myoinositol di- and mono-phosphates (Ullah, 1988). Phytase-producing microorganisms are comprised of bacteria such as *Bacillus subtilis* (Powar and Jagannathan, 1982) and *Pseudomonas* (Cosgrove, 1970); yeasts such as *Saccharomyces cerevisiae* (Nayini and Markakis, 1984); and fungi such as *Aspergillus terreus* (Yamada *et al.*, 1968).

Acid phosphatases are enzymes that catalytically hydrolyze a wide variety of phosphate esters and usually exhibit pH optima below 6.0 (Igarashi & Hollander, 1968). *E.g.*, #EC 3.1.3.2 enzymes catalyze the hydrolysis of orthophosphoric monoesters to orthophosphate products. An acid phosphatase has reportedly been purified from *A. ficuum*. The deglycosylated form of the acid phosphatase has an apparent molecular weight of 32.6 kDa (Ullah *et al.*, 1987).

Phytase and less specific acid phosphatases are produced by the fungus *Aspergillus ficuum* as extracellular enzymes (Shieh *et al.*, 1969). Ullah reportedly purified a phytase from wild-type *A. ficuum* that had an apparent molecular weight of 61.7 kDa (on SDS-PAGE; as corrected for glycosylation); pH optima at pH 2.5 and pH 5.5; a  $K_m$  of about 40  $\mu$ m; and, a specific activity of about 50 U/mg (Ullah, 1988). PCT patent application WO 91/05053 also reportedly discloses isolation and molecular cloning of a phytase from *Aspergillus ficuum* with pH optima at pH 2.5 and pH 5.5, a  $K_m$  of about 250  $\mu$ m, and specific activity of about 100 U/mg protein.

Summarily, the specific activity cited for these previously reported microbial enzymes has been approximately in the range of 50-100 U/mg protein. In contrast, the phytase activity disclosed in the instant invention has been measured to be approximately 4400 U/mg. This corresponds to about a 40-fold or better improvement in activity.

### **2.3 - Solving the Problem of Insufficient Phytate Hydrolysis**

**2.3.1 - Enzyme Additives in Commercial Applications:** The possibility of using microbes capable of producing phytase as a feed additive for monogastric animals has been reported previously (USPN 3,297,548 Shieh and Ware; Nelson *et al.*, 1971). The cost-effectiveness of this approach has been a major limitation for this and other commercial applications. Therefore improved phytase molecules are highly desirable.

Microbial phytases may also reportedly be useful for producing animal feed from certain industrial processes, *e.g.*, wheat and corn waste products. In one aspect, the wet milling process of corn produces glutens sold as animal feeds. The addition of phytase may reportedly improve the nutritional value of the feed product. For example, the use of fungal phytase enzymes and process conditions ( $t \sim 50^{\circ}\text{C}$  and  $\text{pH} \sim 5.5$ ) have been reported previously in (*e.g.* EP 0 321 004). Briefly, in processing soybean meal using traditional steeping methods, *i.e.*, methods without the addition of exogenous phytase enzyme, the presence of unhydrolyzed phytate reportedly renders the meal and wastes unsuitable for feeds used in rearing fish, poultry and other non-ruminants as well as calves fed on milk. Phytase is reportedly useful for improving the nutrient and commercial value of this high protein soy material (see Finase Enzymes by Alko, Rajamäki, Finland). A combination of fungal phytase and a pH 2.5 optimum acid phosphatase from *A. niger* has been used by Alko, Ltd as an animal feed supplement in their phytic acid degradative product Finas F and Finase S. However, the cost-effectiveness of this approach has remained a major limitation to more widespread use. Thus a cost-effective source of phytase would greatly enhance the value of soybean meals as an animal feed (Shieh *et al.*, 1969).

**2.3.2 - Optimization of Enzyme Additives Is Needed:** To solve the problems disclosed, the treatment of foodstuffs with exogenous phytase enzymes has been proposed, but this approach was not been fully optimized, particularly with respect to feasibility and cost efficiency. This optimization requires the consideration that a wide range of applications exists, particularly for large scale production. For example, there is a wide range of foodstuffs, preparation methods thereof, and species of recipient organisms.

In a particular exemplification, it is appreciated that the manufacture of fish feed pellets requires exposure of ingredients to high temperatures &/or pressure in order to produce pellets that do not dissolve &/or degrade prematurely (*e.g. e.g.* prior to consumption) upon subjection to water. It would thus be desirable for this manufacturing process to obtain additive enzymes that are stable under high temperature and/or pressure conditions. Accordingly it is appreciated that distinct phytases may be differentially preferable or optimal for distinct applications.

It is furthermore recognized that an important way to optimize an enzymatic process is through the modification and improvement of the pivotal catalytic enzyme. For example, a transgenic plant can be formed that is comprised of an expression system for expressing a phytase molecule. It is appreciated that by attempting to improve factors that are not directly related to the activity of the expressed molecule proper, such as the expression level, only a finite - and potentially insufficient - level of optimization may be maximally achieved. Accordingly, there is also a need for obtaining molecules with improved characteristics.

A particular way to achieve improvements in the characteristics of a molecule is through a technological approach termed directed evolution, including Diversa Corporation's proprietary approaches for which the term DirectEvolution® has been coined and registered. These approaches are further elaborated in Diversa's co-owned patent (US 5,830,696) as well as in several co-pending patent applications. In brief, DirectEvolution® comprises: a) the subjection of one or more molecular template to mutagenesis to generate novel molecules, and b) the selection among these progeny species of novel molecules with more desirable characteristics.

However, the power of directed evolution depends on the starting choice of starting templates, as well as on the mutagenesis process(es) chosen and the screening process(es) used. For example, the approach of generating and evaluating a full range of mutagenic permutations on randomly chosen molecular templates &/or on initial molecular templates having overly suboptimal properties is often a forbiddingly large task. The use of such templates offers, at best, a circuitously suboptimal path and potentially provides very poor prospects of yielding sufficiently improved progeny molecules. Additionally, it is appreciated that our current body of knowledge is very limited with respect to the ability to rigorously predict beneficial modifications.

Consequently, it is a desirable approach to discover and to make use of molecules that have pre-evolved properties – preferably pre-evolved enzymatic advantages – in nature. It is thus appreciated in the instant disclosure that nature provides (through what has sometimes been termed “natural evolution”) molecules that can be used immediately in commercial applications, or that alternatively, can be subjected to directed evolution to achieve even greater improvements.

In sum, there is a need for novel, highly active, physiologically effective, and economical sources of phytase activity. Specifically, there is a need to identify novel phytases that: a) have superior activities under one or more specific applications, and are thus serviceable for optimizing these specific applications; b) are serviceable as templates for directed evolution to achieve even further improved novel molecules; and c) are serviceable as tools for the identification of additional related molecules by means such as hybridization-based approaches. This invention meets these needs in a novel way.

### **3. SUMMARY OF THE INVENTION**

The present invention provides a polynucleotide and a polypeptide encoded thereby which has been identified as a phytase enzyme having phytase activity. In accordance with one aspect of the present invention, there is provided a novel recombinant enzyme, as well as active fragments, analogs and derivatives thereof.

More particularly, this invention relates to the use of recombinant phytase molecules of bacterial origin that are serviceable for improving the nutritional value of phytate-containing foodstuffs. Previous publications have disclosed the use of fungal phytases, but the use of bacterial phytases for this purpose is novel.

More particularly still, this invention relates to the use of newly identified recombinant phytase molecules of *E.coli* origin that are serviceable for improving the nutritional value of phytate-containing foodstuffs.

This use is comprised of employing the newly identified molecules to hydrolyze phytate in foodstuffs. Hydrolysis may occur before ingestion or after ingestion or both before and after ingestion of the phytate. This application is particularly relevant, but not limited, to non-ruminant organisms and includes the expression of the disclosed novel phytase molecules in transformed hosts, the contacting of the disclosed novel phytase molecules with phytate in foodstuffs and other materials, and the treatment of animal digestive systems with the disclosed novel phytase molecules.

Additionally, hydrolysis may occur independently of consumption, *e.g.* in an *in vitro* application, such as in a reaction vessel. Thus, the treatment of phytate-containing materials includes the treatment of a wide range of materials, including ones that are not intended to be foodstuffs, *e.g.* the treatment of excrementary (or fecal) material.

Preferred molecules of the present invention include a recombinant phytase isolated from *Escherichia coli* B that improves the efficiency of release of phosphorous from phytate and the salts of phytic acid when compared to previously identified fungal phytases.

In accordance with one aspect of the present invention, there is provided a phytase enzyme that is serviceable for incorporation into foodstuffs. More specifically, there is provided a phytase enzyme that is serviceable for improving the nutritional value of phytate-containing foodstuffs. More specifically still, there is provided a phytase enzyme that, when applied to phytate-containing foodstuffs, measurably

improves the growth performance of an organism that consumes it. It is theorized that the beneficial mechanism of action of the phytase activity is comprised appreciably if not substantially of the hydrolysis of phytate. It is provided that the beneficial action may occur before injection or alternatively after injection or alternatively both before and after injection of the phytate-containing foodstuff. In the case where the beneficial action occurs after injection, it is an object of the present invention to provide a phytase enzyme that has activity that is retained upon consumption by non-ruminant organisms.

In accordance with another aspect of the present invention there are provided isolated nucleic acid molecules encoding the enzyme of the present invention - including mRNA, DNA, cDNA, genomic DNA - as well as active derivatives, analogs and fragments of such enzyme.

In accordance with yet a further aspect of the present invention, there is provided a process for producing such polypeptides by recombinant techniques comprising culturing recombinant prokaryotic and/or eukaryotic host cells, containing a nucleic acid sequence encoding an enzyme of the present invention, under conditions promoting expression of said enzyme and subsequent recovery of said enzyme.

In accordance with yet a further aspect of the present invention, there is provided a process for expressing such enzymes, or polynucleotides encoding such enzymes in transgenic plants or plant organs and methods for the production of such plants. This is achievable by introducing into a plant an expression construct comprised of a nucleic acid sequence encoding such phytase enzymes.

In accordance with yet a further aspect of the present invention, there is provided a process for utilizing such enzymes, or polynucleotides encoding such enzymes for use in commercial processes, such as, for example, processes that liberate minerals from phytates in plant materials either *in vitro*, *i.e.*, in feed treatment processes, or *in vivo*, *i.e.*, by administering the enzymes to animals.

In accordance with yet a further aspect of the present invention, there are provided foodstuffs made by the disclosed feed treatment processes.

In accordance with yet a further aspect of the present invention, there are provided a processes for utilizing such enzymes, or polynucleotides encoding such enzymes, for *in vitro* purposes related to research, discovery, and development. In a non-limiting exemplification, such processes comprise the generation of probes for identifying and isolating similar sequences which might encode similar enzymes from other organisms.

In a particular non-limiting exemplification, there are also provided processes for generating nucleic acid probes comprising nucleic acid molecules of sufficient length to specifically hybridize to a nucleic acid sequence of the present invention. By way of preferred exemplification, hybridization-based uses of these probes include, but are by no means limited to, PCR, Northern and Southern types of hybridizations, RNA protection assays, and in situ types of hybridizations. The uses of the instantly disclosed molecules further include, in a non-limiting manner, diagnostic applications.

In accordance with a non-limiting exemplification, these processes comprise the generation of antibodies to the disclosed molecules, and uses of such antibodies, including, for example, for the identification and isolation of similar sequences in enzymes from other organisms. In another non-limiting exemplification, these processes include the use of the present enzymes as templates for directed evolution, comprising the generation of novel molecules by followed by screening-based approaches for discovering of progeny molecules with improved properties.

Also provided is a transgenic non-human organism whose genome comprises a heterologous nucleic acid sequence encoding a polypeptide having phytase activity, wherein said transgene results in expression of a phytase polypeptide.

These and other aspects of the present invention should be apparent to those skilled in the art from the teachings herein.

#### 4. BRIEF DESCRIPTION OF THE DRAWINGS

The following drawings are illustrative of embodiments of the invention and are not meant to limit the scope of the invention as encompassed by the claims.

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Figures 1A and B show the nucleotide and deduced amino acid sequences the enzyme of the present invention. Sequencing was performed using a 378 automated DNA sequencer (Applied Biosystems, Inc.).

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Figure 2 shows the pH and temperature profile and stability data for the phytase enzyme of the present invention. The assay used for these analysis is the following for the detection of phytase activity: Phytase activity is measured by incubating 150μl of the enzyme preparation with 600μl of 2 mM sodium phytate in 100 mM Tris HCl buffer pH 7.5, supplemented with 1mM CaCl<sub>2</sub> for 30 minutes at 37°C. After incubation the reaction is stopped by adding 750μl of 5% trichloroacetic acid. Phosphate released was measured against phosphate standard spectrophotometrically at 700nm after adding 1500μl of the color reagent (4 volumes of 1.5% ammonium molybdate in 5.5% sulfuric acid and 1 volume of 2.7% ferrous sulfate; Shimizu, 1992). OD at 700nm is indicated on the Y-axis of the graphs in Figure 2. Temperature or pH is indicated on the X-axis of the graphs.

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#### 5. DEFINITIONS OF TERMS

In order to facilitate understanding of the examples provided herein, certain frequently occurring methods and/or terms will be described. In addition, the headings and sub-headings used herein are provided for the convenience of the reader and are not to be construed to limit the invention in any manner whatsoever.

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The term “antibody,” as used herein, refers to intact immunoglobulin molecules, as well as fragments of immunoglobulin molecules, such as Fab, Fab', (Fab')<sub>2</sub>, Fv, and SCA fragments, that are capable of binding to an epitope of a phytase polypeptide. These antibody fragments, which retain some ability to selectively bind to the antigen (e.g., an phytase antigen) of the antibody from which they are derived, can be made



using well known methods in the art (see, *e.g.*, Harlow and Lane, *supra*), and are described further, as follows.

(1) An Fab fragment consists of a monovalent antigen-binding fragment of an antibody molecule, and can be produced by digestion of a whole antibody molecule with the enzyme papain, to yield a fragment consisting of an intact light chain and a portion of a heavy chain.

(2) An Fab' fragment of an antibody molecule can be obtained by treating a whole antibody molecule with pepsin, followed by reduction, to yield a molecule consisting of an intact light chain and a portion of a heavy chain. Two Fab' fragments are obtained per antibody molecule treated in this manner.

(3) An (Fab')<sub>2</sub> fragment of an antibody can be obtained by treating a whole antibody molecule with the enzyme pepsin, without subsequent reduction. A (Fab')<sub>2</sub> fragment is a dimer of two Fab' fragments, held together by two disulfide bonds.

(4) An Fv fragment is defined as a genetically engineered fragment containing the variable region of a light chain and the variable region of a heavy chain expressed as two chains.

(5) An single chain antibody (“SCA”) is a genetically engineered single chain molecule containing the variable region of a light chain and the variable region of a heavy chain, linked by a suitable, flexible polypeptide linker.

The term “degrading effective” amount refers to the amount of enzyme which is required to degrade at least 50% of the phytate, as compared to phytate not contacted with the enzyme. Preferably, at least 80% of the phytate is degraded.

“Digestion” of DNA refers to catalytic cleavage of the DNA with a restriction enzyme that acts only at certain sequences in the DNA. The various restriction

enzymes used herein are commercially available and their reaction conditions, cofactors and other requirements were used as would be known to the ordinarily skilled artisan. For analytical purposes, typically 1 µg of plasmid or DNA fragment is used with about 2 units of enzyme in about 20 µl of buffer solution. For the purpose of isolating DNA fragments for plasmid construction, typically 5 to 50 µg of DNA are digested with 20 to 250 units of enzyme in a larger volume. Appropriate buffers and substrate amounts for particular restriction enzymes are specified by the manufacturer. Incubation times of about 1 hour at 37°C are ordinarily used, but may vary in accordance with the supplier's instructions. After digestion the reaction is electrophoresed directly on a gel to isolate the desired fragment.

As used in this invention, the term “epitope” refers to an antigenic determinant on an antigen, such as a phytase polypeptide, to which the paratope of an antibody, such as an phytase-specific antibody, binds. Antigenic determinants usually consist of chemically active surface groupings of molecules, such as amino acids or sugar side chains, and can have specific three-dimensional structural characteristics, as well as specific charge characteristics.

The terms “fragment”, “derivative” and “analog” when referring to the enzyme of Figure 1 comprise a enzyme which retains at least one biological function or activity that is at least essentially same as that of the reference enzyme. Furthermore, the terms “fragment”, “derivative” or “analog” are exemplified by a “pro-form” molecule, such as a low activity proprotein that can be modified by cleavage to produce a mature enzyme with significantly higher activity.

The term “gene” means the segment of DNA involved in producing a polypeptide chain; it includes regions preceding and following the coding region (leader and trailer) as well as intervening sequences (introns) between individual coding segments (exons).

The term “isolated” means that the material is removed from its original environment (*e.g.*, the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or enzyme present in a living animal is not isolated,

but the same polynucleotide or enzyme, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector and/or such polynucleotides or enzymes could be part of a composition, and still be isolated in that such vector or composition is not part of its natural environment.

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By “isolated nucleic acid” is meant a nucleic acid, *e.g.*, a DNA or RNA molecule, that is not immediately contiguous with the 5' and 3' flanking sequences with which it normally is immediately contiguous when present in the naturally occurring genome of the organism from which it is derived. The term thus describes, for example, a nucleic acid that is incorporated into a vector, such as a plasmid or viral vector; a nucleic acid that is incorporated into the genome of a heterologous cell (or the genome of a homologous cell, but at a site different from that at which it naturally occurs); and a nucleic acid that exists as a separate molecule, *e.g.*, a DNA fragment produced by PCR amplification or restriction enzyme digestion, or an RNA molecule produced by *in vitro* transcription. The term also describes a recombinant nucleic acid that forms part of a hybrid gene encoding additional polypeptide sequences that can be used, for example, in the production of a fusion protein.

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“Ligation” refers to the process of forming phosphodiester bonds between two double stranded nucleic acid fragments (Sambrook *et al.*, 1989). Unless otherwise provided, ligation may be accomplished using known buffers and conditions with 10 units of T4 DNA ligase (“ligase”) per 0.5 µg of approximately equimolar amounts of the DNA fragments to be ligated.

25

As used herein, a “nucleic acid molecule” is comprised of at least one nucleotide base or one nucleotide base pair, depending on whether it is single-stranded or double-stranded, respectively. Furthermore, a nucleic acid molecule may belong exclusively or chimerically to any group of nucleotide-containing molecules, as exemplified by, but not limited to, the following groups of nucleic acid molecules:

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RNA, DNA, genomic nucleic acids, non-genomic nucleic acids, naturally occurring and not naturally occurring nucleic acids, and synthetic nucleic acids. This includes, by way of non-limiting example, nucleic acids associated with any organelle, such as the mitochondria, ribosomal RNA, and nucleic acid molecules comprised chimerically of

one or more components that are not naturally occurring along with naturally occurring components.

Additionally, a “nucleic acid molecule” may contain in part one or more non-nucleotide-based components as exemplified by, but not limited to, amino acids and sugars. Thus, by way of example, but not limitation, a ribozyme that is in part nucleotide-based and in part protein-based is considered a “nucleic acid molecule”.

In addition, by way of example, but not limitation, a nucleic acid molecule that is labeled with a detectable moiety, such as a radioactive or alternatively a non-radioactive label, is likewise considered a “nucleic acid molecule”.

The terms “nucleic acid sequence coding for” or a “DNA coding sequence of” or a “nucleotide sequence encoding” a particular enzyme – as well as other synonymous terms – refer to a DNA sequence which is transcribed and translated into an enzyme when placed under the control of appropriate regulatory sequences. A “promotor sequence” is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3’ direction) coding sequence. The promoter is part of the DNA sequence. This sequence region has a start codon at its 3’ terminus. The promoter sequence does include the minimum number of bases where elements necessary to initiate transcription at levels detectable above background bind. However, after the RNA polymerase binds the sequence and transcription is initiated at the start codon (3’ terminus with a promoter), transcription proceeds downstream in the 3’ direction. Within the promotor sequence will be found a transcription initiation site (conveniently defined by mapping with nuclease S1) as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase.

The terms “nucleic acid encoding an enzyme (protein)” or “DNA encoding an enzyme (protein)” or “polynucleotide encoding an enzyme (protein)” and other synonymous terms encompasses a polynucleotide which includes only coding sequence for the enzyme as well as a polynucleotide which includes additional coding and/or non-coding sequence.

In one preferred embodiment, a “specific nucleic acid molecule species” is defined by its chemical structure, as exemplified by, but not limited to, its primary sequence. In another preferred embodiment, a specific “nucleic acid molecule species” is defined by a function of the nucleic acid species or by a function of a product derived from the nucleic acid species. Thus, by way of non-limiting example, a “specific nucleic acid molecule species” may be defined by one or more activities or properties attributable to it, including activities or properties attributable its expressed product.

The instant definition of “assembling a working nucleic acid sample into a nucleic acid library” includes the process of incorporating a nucleic acid sample into a vector-based collection, such as by ligation into a vector and transformation of a host. A description of relevant vectors, hosts, and other reagents as well as specific non-limiting examples thereof are provided hereinafter. The instant definition of “assembling a working nucleic acid sample into a nucleic acid library” also includes the process of incorporating a nucleic acid sample into a non-vector-based collection, such as by ligation to adaptors. Preferably the adaptors can anneal to PCR primers to facilitate amplification by PCR.

Accordingly, in a non-limiting embodiment, a “nucleic acid library” is comprised of a vector-based collection of one or more nucleic acid molecules. In another preferred embodiment a “nucleic acid library” is comprised of a non-vector-based collection of nucleic acid molecules. In yet another preferred embodiment a “nucleic acid library” is comprised of a combined collection of nucleic acid molecules that is in part vector-based and in part non-vector-based. Preferably, the collection of molecules comprising a library is searchable and separable according to individual nucleic acid molecule species.

The present invention provides a “nucleic acid construct” or alternatively a “nucleotide construct” or alternatively a “DNA construct”. The term “construct” is used herein to describe a molecule, such as a polynucleotide (*e.g.*, a phytase polynucleotide) may optionally be chemically bonded to one or more additional molecular moieties, such as a vector, or parts of a vector. In a specific - but by no

means limiting - aspect, a nucleotide construct is exemplified by a DNA expression  
DNA expression constructs suitable for the transformation of a host cell.

“Oligonucleotides” refers to either a single stranded polydeoxynucleotide or two  
5 complementary polydeoxynucleotide strands which may be chemically synthesized.  
Such synthetic oligonucleotides may or may not have a 5' phosphate. Those that do not  
will not ligate to another oligonucleotide without adding a phosphate with an ATP in  
the presence of a kinase. A synthetic oligonucleotide will ligate to a fragment that has  
not been dephosphorylated.

10 A coding sequence is “operably linked to” another coding sequence when RNA  
polymerase will transcribe the two coding sequences into a single mRNA, which is then  
translated into a single polypeptide having amino acids derived from both coding  
sequences. The coding sequences need not be contiguous to one another so long as the  
15 expressed sequences are ultimately processed to produce the desired protein.

The term “phytase-specific probe”, in the context of this method of invention,  
refers to probes that bind to nucleic acids encoding phytase polypeptides, or to  
complementary sequences thereof, to a detectably greater extent than to nucleic acids  
20 encoding other enzymes, or to complementary sequences thereof.

In a strict sense, the terms “phytate”, “phytic acid”, and “phytin”, may be  
differentiated as follows: “phytate” refers to an anionic form of phytic acid; “phytic  
acid” refers to inositol hexaphosphate, a compound that occurs naturally in plants,  
25 including particularly plant leaves, and that may serve as a substrate for the enzyme  
phytase; and “phytin” refers to a salt of phytic acid, such as a calcium-magnesium salt  
of phytic acid. It is understood, accordingly, that “phytate”, “phytic acid”, and “phytin”  
are chemically related and interconvertible forms having a shared chemical structure.  
As used herein, therefore, “phytate”, “phytic acid”, and “phytin” are interchangeable  
30 terms in as much as they are highly related, similar, chemically interconvertible, and  
may all (either with or without said chemical interconversion) be subject to degradation  
by the novel phytase enzyme disclosed instantly. Accordingly, where only one of the  
terms “phytate”, “phytic acid”, or “phytin” is used in the descriptions of the methods

disclosed herein, it is understood to function as a representative term that further refers to any substrate of the enzyme phytase including “phytase”, “phytic acid”, and “phytin”.

5 A “polynucleotide” is a molecule composed of 2 or more nucleotide bases or nucleotide base pairs.

A molecule having a “pre-form” or a “pro-form” refers to a molecule that undergoes any combination of one or more covalent and noncovalent chemical  
10 modifications (*e.g.* glycosylation, proteolytic cleavage, dimerization or oligomerization, temperature-induced or pH-induced conformational change, association with a co-factor, etc.) en route to attain a more mature molecular form having a property difference (*e.g.* an increase in activity) in comparison with the reference pro-form molecule. When a precursor molecule in “pre-form” or in “pro-form” is able to  
15 undergo two or more chemical modification (*e.g.* two proteolytic cleavages, or a proteolytic cleavage and a change in glycosylation) en route to the production of a mature molecule, the term “pre-pro-form” may also be used in reference to the precursor molecule. Accordingly, a pre-pro-enzyme is an enzyme in “pre-pro-form”. Likewise, a pre-pro hormone is a hormone in “pre-pro-form”.

20 As used herein, the term “reagent” includes phytase molecules of the instant invention. Preferably, such phytase molecules catalyze the hydrolysis of phytate to inositol and free phosphate with release of minerals from the phytic acid complex. An exemplary phytase molecule is a phytase derived from *Escherichia coli* B. This  
25 exemplary enzyme is shown in Figure 1, SEQ ID NO:2. Additionally, as used herein, the term “reagent” includes substrate reagents molecules of the instant invention, such as phytate molecules. Preferably, such phytate molecules are found in foodstuffs, potential foodstuffs, byproducts of foodstuffs (both *in vitro* byproducts and *in vivo* byproducts, *e.g.* ex vivo reaction products and animal excremental products), precursors  
30 of foodstuffs, and any other source of phytate.

“Recombinant” enzymes refer to enzymes produced by recombinant DNA techniques, *i.e.*, produced from cells transformed by an exogenous DNA construct

encoding the desired enzyme. “Synthetic” enzymes are those prepared by chemical synthesis.

As known in the art “similarity” between two enzymes is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one enzyme to the sequence of a second enzyme. Similarity may be determined by procedures which are well-known in the art, for example, a BLAST program (Basic Local Alignment Search Tool at the National Center for Biological Information).

The members of a pair of molecules (*e.g.*, an antibody-antigen pair or a nucleic acid pair) are said to “specifically bind” to each other if they bind to each other with greater affinity than to other, non-specific molecules. For example, an antibody raised against an antigen to which it binds more efficiently than to a non-specific protein can be described as specifically binding to the antigen. (Similarly, a nucleic acid probe can be described as specifically binding to a nucleic acid target if it forms a specific duplex with the target by base pairing interactions (see above).)

“Stringent hybridization conditions” means hybridization will occur only if there is at least 90% identity, preferably at least 95% identity and most preferably at least 97% identity between the sequences. *See* Sambrook *et al.*, 1989, which is hereby incorporated by reference in its entirety.

Also included in the invention are polypeptides having sequences that are “substantially identical” to the sequence of a phytase polypeptide, such as one of SEQ ID NO:1. A “substantially identical” amino acid sequence is a sequence that differs from a reference sequence or sequences only by conservative amino acid substitutions, for example, substitutions of one amino acid for another of the same class (*e.g.*, substitution of one hydrophobic amino acid, such as isoleucine, valine, leucine, or methionine, for another, or substitution of one polar amino acid for another, such as substitution of arginine for lysine, glutamic acid for aspartic acid, or glutamine for asparagine).



Additionally a “substantially identical” amino acid sequence is a sequence that differs from a reference sequence or sequences or by one or more non-conservative substitutions, deletions, or insertions, particularly when such a substitution occurs at a site that is not the active site the molecule, and provided that the polypeptide essentially retains its behavioural properties. For example, one or more amino acids can be deleted from a phytase polypeptide, resulting in modification of the structure of the polypeptide, without significantly altering its biological activity. For example, amino- or carboxyl-terminal amino acids that are not required for phytase biological activity can be removed. Such modifications can result in the development of smaller active phytase polypeptides.

The present invention provides a “substantially pure enzyme”. The term “substantially pure enzyme” is used herein to describe a molecule, such as a polypeptide (*e.g.*, a phytase polypeptide, or a fragment thereof) that is substantially free of other proteins, lipids, carbohydrates, nucleic acids, and other biological materials with which it is naturally associated. For example, a substantially pure molecule, such as a polypeptide, can be at least 60%, by dry weight, the molecule of interest. The purity of the polypeptides can be determined using standard methods including, *e.g.*, polyacrylamide gel electrophoresis (*e.g.*, SDS-PAGE), column chromatography (*e.g.*, high performance liquid chromatography (HPLC)), and amino-terminal amino acid sequence analysis.

## 6. DETAILED DESCRIPTION OF THE INVENTION

### 6.1 - Novel Phytase

**6.1.1 - Novel phytase – general overview:** The present invention provides purified a recombinant phytase enzyme, shown in Figure 1. Additionally, the present invention provides isolated nucleic acid molecules (polynucleotides) which encode for the mature enzyme having the deduced amino acid sequence of Figure 1.

The phytase molecules of the instant invention (particularly the recombinant enzyme and the polynucleotides that encode it) are patentably novel with respect to

their structures and with respect to their origin. Additionally, the instant phytase molecules are patentably novel with respect to activity. For example, using an assay (as described in Food Chemicals Codex, 4<sup>th</sup> Ed.) the activity of the instant phytase enzyme was demonstrated to be far superior in comparison to a fungal (*Aspergillus*) phytase control. Specifically, a plurality of experiments showed the *E. coli* phytase to have an activity of about 4400 units/mg and the *Aspergillus* phytase to have an activity of about 105 units/mg. This corresponds to more than a 40-fold difference in activity.

**6.1.2 - Phytase polypeptides:** The present invention provides purified a recombinant enzyme that catalyzes the hydrolysis of phytate to inositol and free phosphate with release of minerals from the phytic acid complex. An exemplary purified enzyme is a phytase derived from *Escherichia coli* B. This exemplary enzyme is shown in Figure 1, SEQ ID NO:2.

The enzymes of the present invention include, in addition to an enzyme of Figure 1 (in particular the mature enzyme), polypeptides having sequences that are “substantially identical” to the sequence of a phytase polypeptide, such as one of SEQ ID 1.

In one embodiment, the phytase enzyme of SEQ ID NO:2 of the present invention has a molecular weight of about 47,056 kilodaltons as measured by SDS-PAGE and inferred from the nucleotide sequence of the gene. The pI is 6.70. The pH and temperature profile and stability data for this enzyme is presented in Figure 2. This purified enzyme may be used to catalyze the hydrolysis of phytate to inositol and free phosphate where desired. The phytase enzyme of the present invention has a high thermostability; thus it is particularly serviceable for raised temperature and/or pressure applications including, but not limited to, the preparation of fish foodstuff pellets that will not dissolve prematurely in water.

The phytase polypeptide included in the invention can have the amino acid sequences of the phytase shown in Figure 1 (SEQ ID NO:2). Phytase polypeptides, such as those isolated from *E. coli* B, can be characterized by catalyzing the hydrolysis

of phytate to inositol and free phosphate with the release of minerals from the phytic acid complex.

Other phytase polypeptides included in the invention are polypeptides having amino acid sequences that are at least about 50% identical to the amino acid sequence of a phytase polypeptide, such as any of the phytase in SEQ ID NO:2. The length of comparison in determining amino acid sequence homology can be, for example, at least 15 amino acids, and for example, at least 20, 25, or 35 amino acids.

Homology or identity is often measured using sequence analysis software (*e.g.*, Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705). Such software matches similar sequences by assigning degrees of homology to various deletions, substitutions and other modifications. The terms “homology” and “identity” in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same when compared and aligned for maximum correspondence over a comparison window or designated region as measured using any number of sequence comparison algorithms or by manual alignment and visual inspection.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared, however a database of reference sequences can be used. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A “comparison window”, as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous

positions after the two sequences are optimally aligned. Methods of alignment of sequence for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482, 1981, by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol 48:443, 1970, by the search for similarity method of person & Lipman, Proc. Nat'l. Acad. Sci. USA 85:2444, 1988, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection. Other algorithms for determining homology or identity include, for example, in addition to a BLAST program (Basic Local Alignment Search Tool at the National Center for Biological Information), ALIGN, AMAS (Analysis of Multiply Aligned Sequences), AMPS (Protein Multiple Sequence Alignment), ASSET (Aligned Segment Statistical Evaluation Tool), BANDS, BESTSCOR, BIOSCAN (Biological Sequence Comparative Analysis Node), BLIMPS (BBlocks IMProved Searcher), FASTA, Intervals & Points, BMB, CLUSTAL V, CLUSTAL W, CONSENSUS, LCONSENSUS, WCONSENSUS, Smith-Waterman algorithm, DARWIN, Las Vegas algorithm, FNAT (Forced Nucleotide Alignment Tool), Framealign, Framesearch, DYNAMIC, FILTER, FSAP (Fristensky Sequence Analysis Package), GAP (Global Alignment Program), GENAL, GIBBS, GenQuest, ISSC (Sensitive Sequence Comparison), LALIGN (Local Sequence Alignment), LCP (Local Content Program), MACAW (Multiple Alignment Construction & Analysis Workbench), MAP (Multiple Alignment Program), MBLKP, MBLKN, PIMA (Pattern-Induced Multi-sequence Alignment), SAGA (Sequence Alignment by Genetic Algorithm) and WHAT-IF. Such alignment programs can also be used to screen genome databases to identify polynucleotide sequences having substantially identical sequences. A number of genome databases are available, for example, a substantial portion of the human genome is available as part of the Human Genome Sequencing Project (J. Roach, [http://weber.u.Washington.edu/~roach/human\\_genome\\_progress2.html](http://weber.u.Washington.edu/~roach/human_genome_progress2.html)) (Gibbs, 1995). At least twenty-one other genomes have already been sequenced, including, for example, *M. genitalium* (Fraser *et al.*, 1995), *M. jannaschii* (Bult *et al.*, 1996), *H. influenzae* (Fleischmann *et al.*, 1995), *E. coli* (Blattner *et al.*, 1997), and yeast (*S. cerevisiae*) (Mewes *et al.*, 1997), and *D. melanogaster* (Adams *et al.*, 2000). Significant progress has also been made in sequencing the genomes of model organism,

such as mouse, *C. elegans*, and *Arabidopsis sp.* Several databases containing genomic information annotated with some functional information are maintained by different organization, and are accessible via the internet, for example, <http://www.tigr.org/tdb>; <http://www.genetics.wisc.edu>; <http://genome-www.stanford.edu/~ball>; <http://hiv-web.lanl.gov>; <http://www.ncbi.nlm.nih.gov>; <http://www.ebi.ac.uk>; <http://Pasteur.fr/other/biology>; and <http://www.genome.wi.mit.edu>.

One example of a useful algorithm is BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, Nuc. Acids Res. 25:3389-3402, 1977, and Altschul *et al.*, J. Mol. Biol. 215:403-410, 1990, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectations (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA 89:10915, 1989) alignments (B) of 50, expectation (E) of 10, M=5, N= -4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, *e.g.*, Karlin & Altschul, Proc. Natl. Acad. Sci. USA 90:5873,

1993). One measure of similarity provided by BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a references sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001.

In one embodiment, protein and nucleic acid sequence homologies are evaluated using the Basic Local Alignment Search Tool ("BLAST") In particular, five specific BLAST programs are used to perform the following task:

- (1) BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;
- (2) BLASTN compares a nucleotide query sequence against a nucleotide sequence database;
- (3) BLASTX compares the six-frame conceptual translation products of a query nucleotide sequence (both strands) against a protein sequence database;
- (4) TBLASTN compares a query protein sequence against a nucleotide sequence database translated in all six reading frames (both strands); and
- (5) TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are preferably identified (*i.e.*, aligned) by means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet *et al.*, Science 256:1443-1445, 1992; Henikoff and Henikoff, Proteins 17:49-61, 1993). Less preferably, the PAM or PAM250 matrices may also be used (see, *e.g.*, Schwartz and Dayhoff, eds., 1978, *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure*, Washington: National Biomedical Research

Foundation). BLAST programs are accessible through the U.S. National Library of Medicine, *e.g.*, at [www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov).

The parameters used with the above algorithms may be adapted depending on the sequence length and degree of homology studied. In some embodiments, the parameters may be the default parameters used by the algorithms in the absence of instructions from the user.

The present invention further relates to an enzyme which has the deduced amino acid sequence of Figure 1, as well as analogs, derivatives, and fragments of such enzyme.

An analog, derivative, or fragment of the enzyme of Figure 1 may be (a) one in which one or more of the amino acid residues are substituted with an amino acid residue which is not encoded by the genetic code, or (b) one in which one or more of the amino acid residues includes a substituent group, or (c) one in which the mature enzyme is fused with another compound, such as a compound to increase the half-life of the enzyme (for example, polyethylene glycol), or (d) to provide a label or a tag, such as a 6xHis tag or a green fluorescent protein tag, (e) one in which the additional amino acids are fused to the mature enzyme, such as a leader or secretory sequence or a sequence which is employed for purification of the mature enzyme or a proprotein sequence. Such analogs, derivatives, and fragments are deemed to be within the scope of those skilled in the art from the teachings herein.

A variant, *e.g.*, a “fragment”, “analog” or “derivative” enzyme, and reference enzyme may differ in amino acid sequence by one or more substitutions, additions, deletions, fusions and truncations, which may be present in any combination.

Among preferred variants are those that vary from a reference by conservative amino acid substitutions. Such substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr,

exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe, Tyr.

Thus, in a particular non-limiting exemplification, a substitution can be comprised of a substitution of one amino acid by another amino acid with a like property. In another particular non-limiting exemplification, a substitution can be comprised of a substitution of an amino acid by an unlike amino acid, where the change is non-inhibitory or silent or improved with respect to at least one enzyme property.

Additionally, in a non-limiting exemplification, an addition can be comprised of an addition either at the amino or the carboxy terminal of the protein or alternatively between the terminal sites, where the change is change is non-inhibitory or silent or improved with respect to at least one enzyme property.

In another particular non-limiting exemplification, a change can be comprised of a plurality of modifications, including substitutions, additions, deletions, fusions and/or truncations, in the enzyme encoded by the reference polynucleotide (SEQ ID NO:1, such that, irrespective of the effects of the individual modifications, when taken together as a set, the effect of the modifications is non-inhibitory or silent or improved with respect to at least one enzyme property.

Most highly preferred are variants which retain substantially the same biological function and activity as the reference polypeptide from which it varies.

The term “variant” refers to polynucleotides or polypeptides of the invention modified at one or more base pairs, codons, introns, exons, or amino acid residues (respectively) yet still retain the biological activity of a phytase of the invention. Variants can be produced by any number of means including methods such as, for example, error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis,



ligation reassembly, GSSM and any combination thereof as discussed more fully below.

**6.1.3 - Phytase polynucleotides:** In accordance with an aspect of the present invention, there are provided isolated nucleic acid molecules (polynucleotides) which encode for the mature enzyme having the deduced amino acid sequence of Figure 1.

The polynucleotide encoding SEQ ID NO:2 was originally isolated from genomic DNA recovered from *Escherichia coli* B as described below. It contains an open reading frame encoding a protein of 432 amino acid residues.

In accordance with another aspect of the present invention, there is provided an isolated polynucleotide encoding an exemplary enzyme of the present invention (SEQ ID NO:1) comprising the DNA of Figure 1.

The present invention also relates to polynucleotides which differ from the reference polynucleotide such that the changes are silent changes, for example the changes do not alter the amino acid sequence encoded by the polynucleotide. The present invention also relates to nucleotide changes which result in amino acid substitutions, additions, deletions, fusions and truncations in the enzyme encoded by the reference polynucleotide (SEQ ID NO:1). In a preferred aspect of the invention these enzymes retain about the same biological action as the enzyme encoded by the reference polynucleotide.

The invention also provides isolated nucleic acid molecules that encode the phytase polypeptide described above. For example, nucleic acids that encode SEQ ID NO:2 are included in the invention. These nucleic acids can contain naturally occurring nucleotide sequences, or sequences that differ from those of the naturally occurring nucleic acids that encode phytases, but encode the same amino acids, due to the degeneracy of the genetic code. The nucleic acids of the invention can contain DNA or RNA nucleotides, or combinations or modifications thereof. Exemplary nucleic acids of the invention are shown in SEQ ID NO:1.

The polynucleotide of the present invention may be in the form of DNA which DNA includes cDNA, genomic DNA, and synthetic DNA. The DNA may be double-stranded or single-stranded, and if single stranded may be the coding strand or non-coding (anti-sense) strand. The coding sequence which encodes the mature enzyme may be identical to the coding sequences shown in Figure 1 and/or that of the deposited clone (SEQ ID NO:1), or may be a different coding sequence which coding sequence, as a result of the redundancy or degeneracy of the genetic code, encodes the same mature enzyme as the DNA of Figure 1 (*e.g.*, SEQ ID NO:1).

The polynucleotide which encodes for the mature enzyme of Figure 1 (*e.g.*, SEQ ID NO:2) may include, but is not limited to: only the coding sequence for the mature enzyme; the coding sequence for the mature enzyme and additional coding sequence such as a leader sequence or a proprotein sequence; the coding sequence for the mature enzyme (and optionally additional coding sequence) and non-coding sequence, such as introns or non-coding sequence 5' and/or 3' of the coding sequence for the mature enzyme.

The present invention further relates to variants of the hereinabove described polynucleotides which encode for fragments, analogs and derivatives of the enzyme having the deduced amino acid sequence of Figure 1 (*e.g.*, SEQ ID NO:2). The variant of the polynucleotide may be a naturally occurring allelic variant of the polynucleotide or a non-naturally occurring variant of the polynucleotide.

Thus, the present invention includes polynucleotides encoding the same mature enzyme as shown in Figure 1 as well as variants of such polynucleotides which variants encode for a fragment, derivative or analog of the enzyme of Figure 1. Such nucleotide variants include deletion variants, substitution variants and addition or insertion variants.

As hereinabove indicated, the polynucleotide may have a coding sequence which is a naturally occurring allelic variant of the coding sequence shown in Figure 1. As known in the art, an allelic variant is an alternate form of a polynucleotide sequence

which may have a substitution, deletion or addition of one or more nucleotides, which does not substantially alter the function of the encoded enzyme.

As discussed herein, variants can be produced by any number of means including methods such as, for example, error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, ligation reassembly, GSSM and any combination thereof.

In one aspect, a non-stochastic method termed synthetic ligation reassembly (SLR), that is somewhat related to stochastic shuffling, save that the nucleic acid building blocks are not shuffled or concatenated or chimerized randomly, but rather are assembled non-stochastically can be used to create variants.

The SLR method does not depend on the presence of a high level of homology between polynucleotides to be shuffled. The invention can be used to non-stochastically generate libraries (or sets) of progeny molecules comprised of over  $10^{100}$  different chimeras. Conceivably, SLR can even be used to generate libraries comprised of over  $10^{1000}$  different progeny chimeras.

Thus, in one aspect, the invention provides a non-stochastic method of producing a set of finalized chimeric nucleic acid molecules having an overall assembly order that is chosen by design, which method is comprised of the steps of generating by design a plurality of specific nucleic acid building blocks having serviceable mutually compatible ligatable ends, and assembling these nucleic acid building blocks, such that a designed overall assembly order is achieved.

The mutually compatible ligatable ends of the nucleic acid building blocks to be assembled are considered to be "serviceable" for this type of ordered assembly if they enable the building blocks to be coupled in predetermined orders. Thus, in one aspect, the overall assembly order in which the nucleic acid building blocks can be coupled is specified by the design of the ligatable ends and, if more than one assembly step is to

be used, then the overall assembly order in which the nucleic acid building blocks can be coupled is also specified by the sequential order of the assembly step(s). In a one embodiment of the invention, the annealed building pieces are treated with an enzyme, such as a ligase (*e.g.*, T4 DNA ligase) to achieve covalent bonding of the building  
5 pieces.

In a another embodiment, the design of nucleic acid building blocks is obtained upon analysis of the sequences of a set of progenitor nucleic acid templates that serve as a basis for producing a progeny set of finalized chimeric nucleic acid molecules.

10 These progenitor nucleic acid templates thus serve as a source of sequence information that aids in the design of the nucleic acid building blocks that are to be mutagenized, *i.e.* chimerized or shuffled.

In one exemplification, the invention provides for the chimerization of a family  
15 of related genes and their encoded family of related products. In a particular exemplification, the encoded products are enzymes. Enzymes and polypeptides of the invention can be mutagenized in accordance with the methods described herein.

Thus according to one aspect of the invention, the sequences of a plurality of  
20 progenitor nucleic acid templates are aligned in order to select one or more demarcation points, which demarcation points can be located at an area of homology. The demarcation points can be used to delineate the boundaries of nucleic acid building blocks to be generated. Thus, the demarcation points identified and selected in the progenitor molecules serve as potential chimerization points in the assembly of the  
25 progeny molecules.

Typically a serviceable demarcation point is an area of homology (comprised of at least one homologous nucleotide base) shared by at least two progenitor templates, but the demarcation point can be an area of homology that is shared by at least half of  
30 the progenitor templates, at least two thirds of the progenitor templates, at least three fourths of the progenitor templates, and preferably at almost all of the progenitor templates. Even more preferably still a serviceable demarcation point is an area of homology that is shared by all of the progenitor templates.

In a one embodiment, the ligation reassembly process is performed exhaustively in order to generate an exhaustive library. In other words, all possible ordered combinations of the nucleic acid building blocks are represented in the set of finalized chimeric nucleic acid molecules. At the same time, the assembly order (*i.e.* the order of assembly of each building block in the 5' to 3' sequence of each finalized chimeric nucleic acid) in each combination is by design (or non-stochastic). Because of the non-stochastic nature of the method, the possibility of unwanted side products is greatly reduced.

In another embodiment, the method provides that, the ligation reassembly process is performed systematically, for example in order to generate a systematically compartmentalized library, with compartments that can be screened systematically, *e.g.*, one by one. In other words the invention provides that, through the selective and judicious use of specific nucleic acid building blocks, coupled with the selective and judicious use of sequentially stepped assembly reactions, an experimental design can be achieved where specific sets of progeny products are made in each of several reaction vessels. This allows a systematic examination and screening procedure to be performed. Thus, it allows a potentially very large number of progeny molecules to be examined systematically in smaller groups.

Because of its ability to perform chimerizations in a manner that is highly flexible yet exhaustive and systematic as well, particularly when there is a low level of homology among the progenitor molecules, the instant invention provides for the generation of a library (or set) comprised of a large number of progeny molecules. Because of the non-stochastic nature of the instant ligation reassembly invention, the progeny molecules generated preferably comprise a library of finalized chimeric nucleic acid molecules having an overall assembly order that is chosen by design. In a particularly embodiment, such a generated library is comprised of greater than  $10^3$  to greater than  $10^{1000}$  different progeny molecular species.

In one aspect, a set of finalized chimeric nucleic acid molecules, produced as described is comprised of a polynucleotide encoding a polypeptide. According to one

embodiment, this polynucleotide is a gene, which may be a man-made gene. According to another embodiment, this polynucleotide is a gene pathway, which may be a man-made gene pathway. The invention provides that one or more man-made genes generated by the invention may be incorporated into a man-made gene pathway, such as  
5 pathway operable in a eukaryotic organism (including a plant).

In another exemplification, the synthetic nature of the step in which the building blocks are generated allows the design and introduction of nucleotides (*e.g.*, one or more nucleotides, which may be, for example, codons or introns or regulatory  
10 sequences) that can later be optionally removed in an *in vitro* process (*e.g.*, by mutagenesis) or in an *in vivo* process (*e.g.*, by utilizing the gene splicing ability of a host organism). It is appreciated that in many instances the introduction of these nucleotides may also be desirable for many other reasons in addition to the potential benefit of creating a serviceable demarcation point.

Thus, according to another embodiment, the invention provides that a nucleic acid building block can be used to introduce an intron. Thus, the invention provides that functional introns may be introduced into a man-made gene of the invention. The invention also provides that functional introns may be introduced into a man-made gene  
15 pathway of the invention. Accordingly, the invention provides for the generation of a chimeric polynucleotide that is a man-made gene containing one (or more) artificially introduced intron(s).

Accordingly, the invention also provides for the generation of a chimeric  
25 polynucleotide that is a man-made gene pathway containing one (or more) artificially introduced intron(s). Preferably, the artificially introduced intron(s) are functional in one or more host cells for gene splicing much in the way that naturally-occurring introns serve functionally in gene splicing. The invention provides a process of producing man-made intron-containing polynucleotides to be introduced into host  
30 organisms for recombination and/or splicing.

A man-made genes produced using the invention can also serve as a substrate for recombination with another nucleic acid. Likewise, a man-made gene pathway

produced using the invention can also serve as a substrate for recombination with another nucleic acid. In a preferred instance, the recombination is facilitated by, or occurs at, areas of homology between the man-made intron-containing gene and a nucleic acid which serves as a recombination partner. In a particularly preferred instance, the recombination partner may also be a nucleic acid generated by the invention, including a man-made gene or a man-made gene pathway. Recombination may be facilitated by or may occur at areas of homology that exist at the one (or more) artificially introduced intron(s) in the man-made gene.

The synthetic ligation reassembly method of the invention utilizes a plurality of nucleic acid building blocks, each of which preferably has two ligatable ends. The two ligatable ends on each nucleic acid building block may be two blunt ends (*i.e.* each having an overhang of zero nucleotides), or preferably one blunt end and one overhang, or more preferably still two overhangs.

A serviceable overhang for this purpose may be a 3' overhang or a 5' overhang. Thus, a nucleic acid building block may have a 3' overhang or alternatively a 5' overhang or alternatively two 3' overhangs or alternatively two 5' overhangs. The overall order in which the nucleic acid building blocks are assembled to form a finalized chimeric nucleic acid molecule is determined by purposeful experimental design and is not random.

According to one preferred embodiment, a nucleic acid building block is generated by chemical synthesis of two single-stranded nucleic acids (also referred to as single-stranded oligos) and contacting them so as to allow them to anneal to form a double-stranded nucleic acid building block.

A double-stranded nucleic acid building block can be of variable size. The sizes of these building blocks can be small or large. Preferred sizes for building block range from 1 base pair (not including any overhangs) to 100,000 base pairs (not including any overhangs). Other preferred size ranges are also provided, which have lower limits of from 1 bp to 10,000 bp (including every integer value in between), and upper limits of from 2 bp to 100,000 bp (including every integer value in between).

Many methods exist by which a double-stranded nucleic acid building block can be generated that is serviceable for the invention; and these are known in the art and can be readily performed by the skilled artisan.

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According to one embodiment, a double-stranded nucleic acid building block is generated by first generating two single stranded nucleic acids and allowing them to anneal to form a double-stranded nucleic acid building block. The two strands of a double-stranded nucleic acid building block may be complementary at every nucleotide apart from any that form an overhang; thus containing no mismatches, apart from any overhang(s). According to another embodiment, the two strands of a double-stranded nucleic acid building block are complementary at fewer than every nucleotide apart from any that form an overhang. Thus, according to this embodiment, a double-stranded nucleic acid building block can be used to introduce codon degeneracy.

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Preferably the codon degeneracy is introduced using the site-saturation mutagenesis described herein, using one or more N,N,G/T cassettes or alternatively using one or more N,N,N cassettes.

The *in vivo* recombination method of the invention can be performed blindly on a pool of unknown hybrids or alleles of a specific polynucleotide or sequence. However, it is not necessary to know the actual DNA or RNA sequence of the specific polynucleotide.

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The approach of using recombination within a mixed population of genes can be useful for the generation of any useful proteins, for example, interleukin I, antibodies, tPA and growth hormone. This approach may be used to generate proteins having altered specificity or activity. The approach may also be useful for the generation of hybrid nucleic acid sequences, for example, promoter regions, introns, exons, enhancer sequences, 3' untranslated regions or 5' untranslated regions of genes. Thus this approach may be used to generate genes having increased rates of expression. This approach may also be useful in the study of repetitive DNA sequences. Finally, this approach may be useful to mutate ribozymes or aptamers.

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In one aspect variants of the polynucleotides and polypeptides described herein are obtained by the use of repeated cycles of reductive reassortment, recombination and selection which allow for the directed molecular evolution of highly complex linear sequences, such as DNA, RNA or proteins thorough recombination.

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*In vivo* shuffling of molecules is useful in providing variants and can be performed utilizing the natural property of cells to recombine multimers. While recombination *in vivo* has provided the major natural route to molecular diversity, genetic recombination remains a relatively complex process that involves 1) the recognition of homologies; 2) strand cleavage, strand invasion, and metabolic steps leading to the production of recombinant chiasma; and finally 3) the resolution of chiasma into discrete recombined molecules. The formation of the chiasma requires the recognition of homologous sequences.

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In a another embodiment, the invention includes a method for producing a hybrid polynucleotide from at least a first polynucleotide and a second polynucleotide. The invention can be used to produce a hybrid polynucleotide by introducing at least a first polynucleotide and a second polynucleotide which share at least one region of partial sequence homology into a suitable host cell. The regions of partial sequence homology promote processes which result in sequence reorganization producing a hybrid polynucleotide. The term "hybrid polynucleotide", as used herein, is any nucleotide sequence which results from the method of the present invention and contains sequence from at least two original polynucleotide sequences. Such hybrid polynucleotides can result from intermolecular recombination events which promote sequence integration between DNA molecules. In addition, such hybrid polynucleotides can result from intramolecular reductive reassortment processes which utilize repeated sequences to alter a nucleotide sequence within a DNA molecule.

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The invention provides a means for generating hybrid polynucleotides which may encode biologically active hybrid polypeptides (*e.g.*, a hybrid phytase). In one aspect, the original polynucleotides encode biologically active polypeptides. The method of the invention produces new hybrid polypeptides by utilizing cellular processes which integrate the sequence of the original polynucleotides such that the

resulting hybrid polynucleotide encodes a polypeptide demonstrating activities derived from the original biologically active polypeptides. For example, the original polynucleotides may encode a particular enzyme from different microorganisms. An enzyme encoded by a first polynucleotide from one organism or variant may, for example, function effectively under a particular environmental condition, *e.g.*, high salinity. An enzyme encoded by a second polynucleotide from a different organism or variant may function effectively under a different environmental condition, such as extremely high temperatures. A hybrid polynucleotide containing sequences from the first and second original polynucleotides may encode an enzyme which exhibits characteristics of both enzymes encoded by the original polynucleotides. Thus, the enzyme encoded by the hybrid polynucleotide may function effectively under environmental conditions shared by each of the enzymes encoded by the first and second polynucleotides, *e.g.*, high salinity and extreme temperatures.

Enzymes encoded by original polynucleotides include, but are not limited to, phytases. A hybrid polypeptide resulting from the method of the invention may exhibit specialized enzyme activity not displayed in the original enzymes. For example, following recombination and/or reductive reassortment of polynucleotides encoding hydrolase activities, the resulting hybrid polypeptide encoded by a hybrid polynucleotide can be screened for specialized hydrolase activities obtained from each of the original enzymes, *i.e.*, the type of bond on which the hydrolase acts and the temperature at which the hydrolase functions. Thus, for example, the hydrolase may be screened to ascertain those chemical functionalities which distinguish the hybrid hydrolase from the original hydrolyases, such as: (a) amide (peptide bonds), *i.e.*, proteases; (b) ester bonds, *i.e.*, esterases and lipases; (c) acetals, *i.e.*, glycosidases and, for example, the temperature, pH or salt concentration at which the hybrid polypeptide functions.

Sources of the original polynucleotides may be isolated from individual organisms ("isolates"), collections of organisms that have been grown in defined media ("enrichment cultures"), or, uncultivated organisms ("environmental samples"). The use of a culture-independent approach to derive polynucleotides encoding novel

bioactivities from environmental samples is most preferable since it allows one to access untapped resources of biodiversity.

“Environmental libraries” are generated from environmental samples and represent the collective genomes of naturally occurring organisms archived in cloning vectors that can be propagated in suitable prokaryotic hosts. Because the cloned DNA is initially extracted directly from environmental samples, the libraries are not limited to the small fraction of prokaryotes that can be grown in pure culture. Additionally, a normalization of the environmental DNA present in these samples could allow more equal representation of the DNA from all of the species present in the original sample. This can dramatically increase the efficiency of finding interesting genes from minor constituents of the sample which may be under-represented by several orders of magnitude compared to the dominant species.

For example, gene libraries generated from one or more uncultivated microorganisms are screened for an activity of interest. Potential pathways encoding bioactive molecules of interest are first captured in prokaryotic cells in the form of gene expression libraries. Polynucleotides encoding activities of interest are isolated from such libraries and introduced into a host cell. The host cell is grown under conditions which promote recombination and/or reductive reassortment creating potentially active biomolecules with novel or enhanced activities.

The microorganisms from which the polynucleotide may be prepared include prokaryotic microorganisms, such as *Xanthobacter*, *Eubacteria* and *Archaeobacteria*, and lower eukaryotic microorganisms such as fungi, some algae and protozoa. Polynucleotides may be isolated from environmental samples in which case the nucleic acid may be recovered without culturing of an organism or recovered from one or more cultured organisms. In one aspect, such microorganisms may be extremophiles, such as hyperthermophiles, psychrophiles, psychrotrophs, halophiles, barophiles and acidophiles. Polynucleotides encoding enzymes isolated from extremophilic microorganisms are particularly preferred. Such enzymes may function at temperatures above 100°C in terrestrial hot springs and deep sea thermal vents, at temperatures below 0°C in arctic waters, in the saturated salt environment of the Dead Sea, at pH values

around 0 in coal deposits and geothermal sulfur-rich springs, or at pH values greater than 11 in sewage sludge. For example, several esterases and lipases cloned and expressed from extremophilic organisms show high activity throughout a wide range of temperatures and pHs.

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Polynucleotides selected and isolated as hereinabove described are introduced into a suitable host cell. A suitable host cell is any cell which is capable of promoting recombination and/or reductive reassortment. The selected polynucleotides are preferably already in a vector which includes appropriate control sequences. The host cell can be a higher eukaryotic cell, such as a mammalian cell, or a lower eukaryotic cell, such as a yeast cell, or preferably, the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-Dextran mediated transfection, or electroporation (Davis *et al.*, 1986).

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As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as *E. coli*, *Streptomyces*, *Salmonella typhimurium*; fungal cells, such as yeast; insect cells such as *Drosophila S2* and *Spodoptera Sf9*; animal cells such as CHO, COS or Bowes melanoma; adenoviruses; and plant cells. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein.

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With particular references to various mammalian cell culture systems that can be employed to express recombinant protein, examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described in "SV40-transformed simian cells support the replication of early SV40 mutants" (Gluzman, 1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

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Host cells containing the polynucleotides of interest can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying genes. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan. The clones which are identified as having the specified enzyme activity may then be sequenced to identify the polynucleotide sequence encoding an enzyme having the enhanced activity.

In another aspect, methods can be used to generate novel polynucleotides encoding biochemical pathways from one or more operons or gene clusters or portions thereof. For example, bacteria and many eukaryotes have a coordinated mechanism for regulating genes whose products are involved in related processes. The genes are clustered, in structures referred to as "gene clusters," on a single chromosome or immediately adjacent to one another and are transcribed together under the control of a single regulatory sequence, including a single promoter which initiates transcription of the entire cluster. Thus, a gene cluster is a group of adjacent genes that are either identical or related, usually as to their function. An example of a biochemical pathway encoded by gene clusters are polyketides. Polyketides are molecules which are an extremely rich source of bioactivities, including antibiotics (such as tetracyclines and erythromycin), anti-cancer agents (daunomycin), immunosuppressants (FK506 and rapamycin), and veterinary products (monensin). Many polyketides (produced by polyketide synthases) are valuable as therapeutic agents. Polyketide synthases are multifunctional enzymes that catalyze the biosynthesis of an enormous variety of carbon chains differing in length and patterns of functionality and cyclization. Polyketide synthase genes fall into gene clusters and at least one type (designated type I) of polyketide synthases have large size genes and enzymes, complicating genetic manipulation and *in vitro* studies of these genes/proteins.

Gene cluster DNA can be isolated from different organisms and ligated into vectors, particularly vectors containing expression regulatory sequences which can control and regulate the production of a detectable protein or protein-related array activity from the ligated gene clusters. Use of vectors which have an exceptionally

large capacity for exogenous DNA introduction are particularly appropriate for use with such gene clusters and are described by way of example herein to include the f-factor (or fertility factor) of *E. coli*. This f-factor of *E. coli* is a plasmid which affects high-frequency transfer of itself during conjugation and is ideal to achieve and stably propagate large DNA fragments, such as gene clusters from mixed microbial samples. Once ligated into an appropriate vector, two or more vectors containing different phytase gene clusters can be introduced into a suitable host cell. Regions of partial sequence homology shared by the gene clusters will promote processes which result in sequence reorganization resulting in a hybrid gene cluster. The novel hybrid gene cluster can then be screened for enhanced activities not found in the original gene clusters.

Therefore, in a one embodiment, the invention relates to a method for producing a biologically active hybrid polypeptide and screening such a polypeptide for enhanced activity by:

- 1) introducing at least a first polynucleotide in operable linkage and a second polynucleotide in operable linkage, said at least first polynucleotide and second polynucleotide sharing at least one region of partial sequence homology, into a suitable host cell;
- 2) growing the host cell under conditions which promote sequence reorganization resulting in a hybrid polynucleotide in operable linkage;
- 3) expressing a hybrid polypeptide encoded by the hybrid polynucleotide;
- 4) screening the hybrid polypeptide under conditions which promote identification of enhanced biological activity; and
- 5) isolating the a polynucleotide encoding the hybrid polypeptide.

Methods for screening for various enzyme activities are known to those of skill in the art and are discussed throughout the present specification. Such methods may be employed when isolating the polypeptides and polynucleotides of the invention.

As representative examples of expression vectors which may be used there may be mentioned viral particles, baculovirus, phage, plasmids, phagemids, cosmids, fosmids, bacterial artificial chromosomes, viral DNA (*e.g.*, vaccinia, adenovirus, fowl

pox virus, pseudorabies and derivatives of SV40), P1-based artificial chromosomes, yeast plasmids, yeast artificial chromosomes, and any other vectors specific for specific hosts of interest (such as bacillus, aspergillus and yeast). Thus, for example, the DNA may be included in any one of a variety of expression vectors for expressing a polypeptide. Such vectors include chromosomal, nonchromosomal and synthetic DNA sequences. Large numbers of suitable vectors are known to those of skill in the art, and are commercially available. The following vectors are provided by way of example; Bacterial: pQE vectors (Qiagen), pBluescript plasmids, pNH vectors, (lambda-ZAP vectors (Stratagene); ptrc99a, pKK223-3, pDR540, pRIT2T (Pharmacia); Eukaryotic: pXT1, pSG5 (Stratagene), pSVK3, pBPV, pMSG, pSVLSV40 (Pharmacia). However, any other plasmid or other vector may be used so long as they are replicable and viable in the host. Low copy number or high copy number vectors may be employed with the present invention.

A preferred type of vector for use in the present invention contains an f-factor origin replication. The f-factor (or fertility factor) in *E. coli* is a plasmid which effects high frequency transfer of itself during conjugation and less frequent transfer of the bacterial chromosome itself. A particularly preferred embodiment is to use cloning vectors, referred to as "fosmids" or bacterial artificial chromosome (BAC) vectors. These are derived from *E. coli* f-factor which is able to stably integrate large segments of genomic DNA. When integrated with DNA from a mixed uncultured environmental sample, this makes it possible to achieve large genomic fragments in the form of a stable "environmental DNA library."

Another type of vector for use in the present invention is a cosmid vector. Cosmid vectors were originally designed to clone and propagate large segments of genomic DNA. Cloning into cosmid vectors is described in detail in "Molecular Cloning: A laboratory Manual" (Sambrook *et al.*, 1989).

The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct RNA synthesis. Particular named bacterial promoters include *lacI*, *lacZ*, *T3*, *T7*, *gpt*, *lambda P<sub>R</sub>*, *P<sub>L</sub>* and *trp*. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early

and late SV40, LTRs from retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression. Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or tetracycline or ampicillin resistance in *E. coli*.

*In vivo* reassortment is focused on “inter-molecular” processes collectively referred to as “recombination” which in bacteria, is generally viewed as a “RecA-dependent” phenomenon. The invention can rely on recombination processes of a host cell to recombine and re-assort sequences, or the cells’ ability to mediate reductive processes to decrease the complexity of quasi-repeated sequences in the cell by deletion. This process of “reductive reassortment” occurs by an “intra-molecular”, RecA-independent process.

Therefore, in another aspect of the invention, variant polynucleotides can be generated by the process of reductive reassortment. The method involves the generation of constructs containing consecutive sequences (original encoding sequences), their insertion into an appropriate vector, and their subsequent introduction into an appropriate host cell. The reassortment of the individual molecular identities occurs by combinatorial processes between the consecutive sequences in the construct possessing regions of homology, or between quasi-repeated units. The reassortment process recombines and/or reduces the complexity and extent of the repeated sequences, and results in the production of novel molecular species. Various treatments may be applied to enhance the rate of reassortment. These could include treatment with ultra-violet light, or DNA damaging chemicals, and/or the use of host cell lines displaying enhanced levels of “genetic instability”. Thus the reassortment process may involve homologous recombination or the natural property of quasi-repeated sequences to direct their own evolution.



Repeated or “quasi-repeated” sequences play a role in genetic instability. In the present invention, “quasi-repeats” are repeats that are not restricted to their original unit structure. Quasi-repeated units can be presented as an array of sequences in a construct; consecutive units of similar sequences. Once ligated, the junctions between the consecutive sequences become essentially invisible and the quasi-repetitive nature of the resulting construct is now continuous at the molecular level. The deletion process the cell performs to reduce the complexity of the resulting construct operates between the quasi-repeated sequences. The quasi-repeated units provide a practically limitless repertoire of templates upon which slippage events can occur. The constructs containing the quasi-repeats thus effectively provide sufficient molecular elasticity that deletion (and potentially insertion) events can occur virtually anywhere within the quasi-repetitive units.

When the quasi-repeated sequences are all ligated in the same orientation, for instance head to tail or vice versa, the cell cannot distinguish individual units. Consequently, the reductive process can occur throughout the sequences. In contrast, when for example, the units are presented head to head, rather than head to tail, the inversion delineates the endpoints of the adjacent unit so that deletion formation will favor the loss of discrete units. Thus, it is preferable with the present method that the sequences are in the same orientation. Random orientation of quasi-repeated sequences will result in the loss of reassortment efficiency, while consistent orientation of the sequences will offer the highest efficiency. However, while having fewer of the contiguous sequences in the same orientation decreases the efficiency, it may still provide sufficient elasticity for the effective recovery of novel molecules. Constructs can be made with the quasi-repeated sequences in the same orientation to allow higher efficiency.

Sequences can be assembled in a head to tail orientation using any of a variety of methods, including the following:

- a) Primers that include a poly-A head and poly-T tail which when made single-stranded would provide orientation can be utilized. This is

accomplished by having the first few bases of the primers made from RNA and hence easily removed RNaseH.

- b) Primers that include unique restriction cleavage sites can be utilized. Multiple sites, a battery of unique sequences, and repeated synthesis and ligation steps would be required.
- c) The inner few bases of the primer could be thiolated and an exonuclease used to produce properly tailed molecules.

The recovery of the re-assorted sequences relies on the identification of cloning vectors with a reduced RI. The re-assorted encoding sequences can then be recovered by amplification. The products are re-cloned and expressed. The recovery of cloning vectors with reduced RI can be effected by:

- 1) The use of vectors only stably maintained when the construct is reduced in complexity.
- 2) The physical recovery of shortened vectors by physical procedures. In this case, the cloning vector would be recovered using standard plasmid isolation procedures and size fractionated on either an agarose gel, or column with a low molecular weight cut off utilizing standard procedures.
- 3) The recovery of vectors containing interrupted genes which can be selected when insert size decreases.
- 4) The use of direct selection techniques with an expression vector and the appropriate selection.

Encoding sequences (for example, genes) from related organisms may demonstrate a high degree of homology and encode quite diverse protein products. These types of sequences are particularly useful in the present invention as quasi-repeats. However, while the examples illustrated below demonstrate the reassortment of nearly identical original encoding sequences (quasi-repeats), this process is not limited to such nearly identical repeats.

The following example demonstrates a method of the invention. Encoding nucleic acid sequences (quasi-repeats) derived from three (3) unique species are depicted. Each sequence encodes a protein with a distinct set of properties. Each of the

sequences differs by a single or a few base pairs at a unique position in the sequence which are designated “A”, “B” and “C”. The quasi-repeated sequences are separately or collectively amplified and ligated into random assemblies such that all possible permutations and combinations are available in the population of ligated molecules.

- 5 The number of quasi-repeat units can be controlled by the assembly conditions. The average number of quasi-repeated units in a construct is defined as the repetitive index (RI).

10 Once formed, the constructs may, or may not be size fractionated on an agarose gel according to published protocols, inserted into a cloning vector, and transfected into an appropriate host cell. The cells are then propagated and “reductive reassortment” is effected. The rate of the reductive reassortment process may be stimulated by the introduction of DNA damage if desired. Whether the reduction in RI is mediated by deletion formation between repeated sequences by an “intra-molecular” mechanism, or  
15 mediated by recombination-like events through “inter-molecular” mechanisms is immaterial. The end result is a reassortment of the molecules into all possible combinations.

20 Optionally, the method comprises the additional step of screening the library members of the shuffled pool to identify individual shuffled library members having the ability to bind or otherwise interact, or catalyze a particular reaction (*e.g.*, such as catalyzing the hydrolysis of a haloalkane).

25 The polypeptides that are identified from such libraries can be used for therapeutic, diagnostic, research and related purposes (*e.g.*, catalysts, solutes for increasing osmolarity of an aqueous solution, and the like), and/or can be subjected to one or more additional cycles of shuffling and/or selection.

30 In another aspect, prior to or during recombination or reassortment, polynucleotides of the invention or polynucleotides generated by the method described herein can be subjected to agents or processes which promote the introduction of mutations into the original polynucleotides. The introduction of such mutations would increase the diversity of resulting hybrid polynucleotides and polypeptides encoded

therefrom. The agents or processes which promote mutagenesis can include, but are not limited to: (+)-CC-1065, or a synthetic analog such as (+)-CC-1065-(N3-Adenine, see Sun and Hurley, 1992); an N-acetylated or deacetylated 4'-fluoro-4-aminobiphenyl adduct capable of inhibiting DNA synthesis (see, for example, van de Poll *et al.*, 1992);  
5 or a N-acetylated or deacetylated 4-aminobiphenyl adduct capable of inhibiting DNA synthesis (see also, van de Poll *et al.*, 1992, pp. 751-758); trivalent chromium, a trivalent chromium salt, a polycyclic aromatic hydrocarbon ("PAH") DNA adduct capable of inhibiting DNA replication, such as 7-bromomethyl-benz[*a*]anthracene ("BMA"), tris(2,3-dibromopropyl)phosphate ("Tris-BP"), 1,2-dibromo-3-  
10 chloropropane ("DBCP"), 2-bromoacrolein (2BA), benzo[*a*]pyrene-7,8-dihydrodiol-9-10-epoxide ("BPDE"), a platinum(II) halogen salt, N-hydroxy-2-amino-3-methylimidazo[4,5-*f*]-quinoline ("N-hydroxy-IQ"), and N-hydroxy-2-amino-1-methyl-6-phenylimidazo[4,5-*f*]-pyridine ("N-hydroxy-PhIP"). Especially preferred means for slowing or halting PCR amplification consist of UV light (+)-CC-1065 and (+)-CC-  
15 1065-(N3-Adenine). Particularly encompassed means are DNA adducts or polynucleotides comprising the DNA adducts from the polynucleotides or polynucleotides pool, which can be released or removed by a process including heating the solution comprising the polynucleotides prior to further processing.

20 In another aspect the invention is directed to a method of producing recombinant proteins having biological activity by treating a sample comprising double-stranded template polynucleotides encoding a wild-type protein under conditions according to the invention which provide for the production of hybrid or re-assorted polynucleotides.

25 The invention also provides for the use of proprietary codon primers (containing a degenerate N,N,N sequence) to introduce point mutations into a polynucleotide, so as to generate a set of progeny polypeptides in which a full range of single amino acid substitutions is represented at each amino acid position (gene site saturated mutagenesis (GSSM)). The oligos used are comprised contiguously of a first homologous sequence,  
30 a degenerate N,N,N sequence, and preferably but not necessarily a second homologous sequence. The downstream progeny translational products from the use of such oligos

include all possible amino acid changes at each amino acid site along the polypeptide, because the degeneracy of the N,N,N sequence includes codons for all 20 amino acids.

In one aspect, one such degenerate oligo (comprised of one degenerate N,N,G/T cassette) is used for subjecting each original codon in a parental polynucleotide template to a full range of codon substitutions. In another aspect, at least two degenerate N,N,G/T cassettes are used – either in the same oligo or not, for subjecting at least two original codons in a parental polynucleotide template to a full range of codon substitutions. Thus, more than one N,N,G/T sequence can be contained in one oligo to introduce amino acid mutations at more than one site. This plurality of N,N,G/T sequences can be directly contiguous, or separated by one or more additional nucleotide sequence(s). In another aspect, oligos serviceable for introducing additions and deletions can be used either alone or in combination with the codons containing an N,N,G/T sequence, to introduce any combination or permutation of amino acid additions, deletions, and/or substitutions.

In a particular exemplification, it is possible to simultaneously mutagenize two or more contiguous amino acid positions using an oligo that contains contiguous N,N,G/T triplets, *i.e.* a degenerate (N,N,G/T)<sub>n</sub> sequence.

In another aspect, the present invention provides for the use of degenerate cassettes having less degeneracy than the N,N,G/T sequence. For example, it may be desirable in some instances to use (*e.g.* in an oligo) a degenerate triplet sequence comprised of only one N, where said N can be in the first second or third position of the triplet. Any other bases including any combinations and permutations thereof can be used in the remaining two positions of the triplet. Alternatively, it may be desirable in some instances to use (*e.g.*, in an oligo) a degenerate N,N,N triplet sequence, or an N,N,G/C triplet sequence.

It is appreciated, however, that the use of a degenerate triplet (such as N,N,G/T or an N,N,G/C triplet sequence) as disclosed in the instant invention is advantageous for several reasons. In one aspect, this invention provides a means to systematically and fairly easily generate the substitution of the full range of possible amino acids (for a

total of 20 amino acids) into each and every amino acid position in a polypeptide. Thus, for a 100 amino acid polypeptide, the invention provides a way to systematically and fairly easily generate 2000 distinct species (*i.e.*, 20 possible amino acids per position times 100 amino acid positions). It is appreciated that there is provided, through the use of an oligo containing a degenerate N,N,G/T or an N,N, G/C triplet sequence, 32 individual sequences that code for 20 possible amino acids. Thus, in a reaction vessel in which a parental polynucleotide sequence is subjected to saturation mutagenesis using one such oligo, there are generated 32 distinct progeny polynucleotides encoding 20 distinct polypeptides. In contrast, the use of a non-degenerate oligo in site-directed mutagenesis leads to only one progeny polypeptide product per reaction vessel.

This invention also provides for the use of nondegenerate oligos, which can optionally be used in combination with degenerate primers disclosed. It is appreciated that in some situations, it is advantageous to use nondegenerate oligos to generate specific point mutations in a working polynucleotide. This provides a means to generate specific silent point mutations, point mutations leading to corresponding amino acid changes, and point mutations that cause the generation of stop codons and the corresponding expression of polypeptide fragments.

Thus, in one embodiment, each saturation mutagenesis reaction vessel contains polynucleotides encoding at least 20 progeny polypeptide molecules such that all 20 amino acids are represented at the one specific amino acid position corresponding to the codon position mutagenized in the parental polynucleotide. The 32-fold degenerate progeny polypeptides generated from each saturation mutagenesis reaction vessel can be subjected to clonal amplification (*e.g.*, cloned into a suitable *E. coli* host using an expression vector) and subjected to expression screening. When an individual progeny polypeptide is identified by screening to display a favorable change in property (when compared to the parental polypeptide), it can be sequenced to identify the correspondingly favorable amino acid substitution contained therein.

It is appreciated that upon mutagenizing each and every amino acid position in a parental polypeptide using saturation mutagenesis as disclosed herein, favorable amino

acid changes may be identified at more than one amino acid position. One or more new progeny molecules can be generated that contain a combination of all or part of these favorable amino acid substitutions. For example, if 2 specific favorable amino acid changes are identified in each of 3 amino acid positions in a polypeptide, the permutations include 3 possibilities at each position (no change from the original amino acid, and each of two favorable changes) and 3 positions. Thus, there are  $3 \times 3 \times 3$  or 27 total possibilities, including 7 that were previously examined - 6 single point mutations (*i.e.*, 2 at each of three positions) and no change at any position.

In yet another aspect, site-saturation mutagenesis can be used together with shuffling, chimerization, recombination and other mutagenizing processes, along with screening. This invention provides for the use of any mutagenizing process(es), including saturation mutagenesis, in an iterative manner. In one exemplification, the iterative use of any mutagenizing process(es) is used in combination with screening.

Thus, in a non-limiting exemplification, polynucleotides and polypeptides of the invention can be derived by saturation mutagenesis in combination with additional mutagenization processes, such as process where two or more related polynucleotides are introduced into a suitable host cell such that a hybrid polynucleotide is generated by recombination and reductive reassortment.

In addition to performing mutagenesis along the entire sequence of a gene, mutagenesis can be used to replace each of any number of bases in a polynucleotide sequence, wherein the number of bases to be mutagenized is preferably every integer from 15 to 100,000. Thus, instead of mutagenizing every position along a molecule, one can subject every or a discrete number of bases (preferably a subset totaling from 15 to 100,000) to mutagenesis. Preferably, a separate nucleotide is used for mutagenizing each position or group of positions along a polynucleotide sequence. A group of 3 positions to be mutagenized may be a codon. The mutations are preferably introduced using a mutagenic primer, containing a heterologous cassette, also referred to as a mutagenic cassette. Preferred cassettes can have from 1 to 500 bases. Each nucleotide position in such heterologous cassettes be N, A, C, G, T, A/C, A/G, A/T,

C/G, C/T, G/T, C/G/T, A/G/T, A/C/T, A/C/G, or E, where E is any base that is not A, C, G, or T (E can be referred to as a designer oligo).

In a general sense, saturation mutagenesis is comprised of mutagenizing a complete set of mutagenic cassettes (wherein each cassette is preferably about 1-500 bases in length) in defined polynucleotide sequence to be mutagenized (wherein the sequence to be mutagenized is preferably from about 15 to 100,000 bases in length). Thus, a group of mutations (ranging from 1 to 100 mutations) is introduced into each cassette to be mutagenized. A grouping of mutations to be introduced into one cassette can be different or the same from a second grouping of mutations to be introduced into a second cassette during the application of one round of saturation mutagenesis. Such groupings are exemplified by deletions, additions, groupings of particular codons, and groupings of particular nucleotide cassettes.

Defined sequences to be mutagenized include a whole gene, pathway, cDNA, an entire open reading frame (ORF), and entire promoter, enhancer, repressor/transactivator, origin of replication, intron, operator, or any polynucleotide functional group. Generally, a "defined sequences" for this purpose may be any polynucleotide that a 15 base-polynucleotide sequence, and polynucleotide sequences of lengths between 15 bases and 15,000 bases (this invention specifically names every integer in between). Considerations in choosing groupings of codons include types of amino acids encoded by a degenerate mutagenic cassette.

In a particularly preferred exemplification a grouping of mutations that can be introduced into a mutagenic cassette, this invention specifically provides for degenerate codon substitutions (using degenerate oligos) that code for 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, and 20 amino acids at each position, and a library of polypeptides encoded thereby.

The present invention also includes polynucleotides, wherein the coding sequence for the mature enzyme may be fused in the same reading frame to a polynucleotide sequence which aids in expression and secretion of an enzyme from a host cell, for example, a leader sequence which functions to control transport of an



enzyme from the cell. An enzyme having a leader sequence is an example of a preprotein and may have the leader sequence cleaved by the host cell to form the mature form of the enzyme. The polynucleotides may also encode for a proprotein which is exemplified by a mature protein plus additional 5' amino acid residues. An otherwise mature protein having a prosequence is exemplified by a proprotein that is an inactive form of the protein. Once the prosequence is cleaved an active mature protein remains.

Thus, for example, the polynucleotide of the present invention may encode for a mature enzyme, or for an enzyme having a prosequence or for an enzyme having both a prosequence and a presequence (*e.g.* leader sequence).

**6.1.4 - Methods of isolation:** The coding sequences for the phytase enzymes of the present invention were identified by preparing *E.coli* B genomic DNA, for example, and recovering (via, for example, PCR amplification) from the genomic DNA, DNA encoding phytase activity. Such methods for recovery are well-known in the art. One means, for example, comprises designing amplification primers to recover the coding sequence, amplifying the gene from the genomic DNA, subcloning the DNA into a vector, transforming the resulting construct into a host strain, and expressing the phytase enzyme for evaluation. Such procedures are well known in the art and methods are provided, for example, in Sambrook *et al.*, 1989, which is hereby incorporated by reference in its entirety.

In a preferred embodiment, the enzyme of the present invention, was isolated from an *E.coli* B genomic DNA by the following technique:  
*E.coli* B genomic DNA was obtained commercially (Sigma: Catalog # D-2001, St. Louis, New Jersey). The following primers were used to amplify the gene directly from the genomic DNA:

5' primer gtttctgaattcaaggaggaatttaaATGAAAGCGATCTTAATCCCATT (SEQ ID

NO:3); and

3' primer gtttctggatccTTACAAACTGCACGCCGGTAT (SEQ ID NO:4)

Pfu polymerase was used according to manufacturers protocol (Stratagene Cloning Systems, Inc., La Jolla, CA).

PCR product and pQE60 vector (Qiagen) were both digested with EcoRI and BglII restriction endonucleases (New England Biolabs) according to manufacturers protocols. Ligation and transformation into, and expression in M15 pREP4 host cells (Qiagen) yields c-term 6X-His tagged protein.

**6.1.5 - Determination of activity:** The isolated nucleic acid sequences and other enzymes may then be measured for retention of biological activity characteristic to the enzyme of the present invention, for example, in an assay for detecting enzymatic phytase activity (Food Chemicals Codex, 4<sup>th</sup> Ed.). Such enzymes include truncated forms of phytase, and variants such as deletion and insertion variants.

An *in vitro* example of such an assay is the following assay for the detection of phytase activity: Phytase activity can be measured by incubating 150µl of the enzyme preparation with 600µl of 2 mM sodium phytate in 100 mM Tris HCl buffer pH 7.5, supplemented with 1mM CaCl<sub>2</sub> for 30 minutes at 37°C. After incubation the reaction is stopped by adding 750µl of 5% trichloroacetic acid. Phosphate released was measured against phosphate standard spectrophotometrically at 700nm after adding 1500µl of the color reagent (4 volumes of 1.5% ammonium molybdate in 5.5% sulfuric acid and 1 volume of 2.7% ferrous sulfate; Shimizu, 1992). One unit of enzyme activity is defined as the amount of enzyme required to liberate one µmol Pi per min under assay conditions. Specific activity can be expressed in units of enzyme activity per mg of protein.

The enzyme of the present invention has enzymatic activity with respect to the hydrolysis of phytate to inositol and free phosphate.

## **6.2 - Production of Novel Phytase**

**6.2.1 - Methods of production - general overview:** The enzymes and polynucleotides of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity. The phytase polypeptide of the invention

can be obtained using any of several standard methods. For example, phytase polypeptides can be produced in a standard recombinant expression system (see below), chemically synthesized (this approach may be limited to small phytase peptide fragments), or purified from organisms in which they are naturally expressed.

- 5 Serviceable recombinant expression methods include the use of mammalian hosts, microbial hosts, and plant hosts.

The recombinant expression of the instant phytase molecules may be achieved in combination with one or more additional molecules such as, for example, other  
10 enzymes. This approach is serviceable for producing combination products, such as a plant or plant part that contains the instant phytase molecules as well as one or more additional molecules – preferably said phytase molecules and said additional molecules are serviceable in a combination treatment. The resulting recombinantly expressed molecules may be used in homogenized and/or purified form or alternatively in  
15 relatively unpurified form (*e.g.* as consumable plant parts that are serviceable when admixed with other foodstuffs for catalyzing the degradation of phytate).

In sum, in a non-limiting embodiment, the present invention provides a recombinant enzyme expressed in a host. In another non-limiting embodiment, the  
20 present invention provides a substantially pure phytase enzyme. Thus, an enzyme of the present invention may be a recombinant enzyme, a natural enzyme, or a synthetic enzyme, preferably a recombinant enzyme.

**6.2.2 - Recombinant expression:** The present invention also relates to vectors  
25 which include polynucleotides of the present invention, host cells which are genetically engineered with vectors of the invention, and the production of enzymes of the invention by recombinant techniques.

Host cells are genetically engineered (*e.g.* transduced or transformed or  
30 transfected) with the vectors containing the polynucleotides of this invention. Such vectors may be, for example, a cloning vector or an expression vector. The vector may be, for example, in the form of a plasmid, a viral particle, a phage, a prion, etc. The engineered host cells can be cultured in conventional nutrient media modified as

appropriate for activating promoters, &/or selecting transformants or amplifying the genes of the present invention. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression, and will be apparent to the ordinarily skilled artisan.

5

The polynucleotides of the present invention may be employed for producing enzymes by recombinant techniques. Thus, for example, the polynucleotide may be included in any one of a variety of expression vectors for expressing an enzyme. Such vectors include chromosomal, nonchromosomal and synthetic DNA sequences, *e.g.*, derivatives of SV40; bacterial plasmids; phage DNA; baculovirus; yeast plasmids; vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies. However, any other vector may be used as long as it is replicable and viable in the host.

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The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is inserted into an appropriate restriction endonuclease site(s) by procedures known in the art. Inclusive in this meaning is the use of blunt-ended molecules which could be generated by the use of restriction digestion as well as restriction digestion-independent means. Alternatively, the insert may be incorporated into a vector by so called "ligase-independent" means. In a particular aspect, a "ligase-independent" means is exemplified by the use of topoisomerase-mediated ligation at room temperature, for example according to the commercially available kit termed TOPO-TA Cloning® (Invitrogen Corporation, Carlsbad, CA). Alternative enzymes, including isomers of topoisomerase as well as more distantly related recombination enzymes (*e.g.* recombinases), may also be serviceable for mediating this type of "ligase-independent" incorporation. In another particular aspect, a "ligase-independent" means is exemplified by the use host repair mechanisms. Such procedures and others are deemed to be within the scope of those skilled in the art.

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The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. As representative examples of such promoters, there may be mentioned: an LTR or SV40

promoter, an *E. coli. lac* or *trp*, a phage lambda P<sub>L</sub> promoter and other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for  
5 amplifying expression.

In addition, the expression vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as  
10 tetracycline or ampicillin resistance in *E. coli*.

The vector containing the appropriate DNA sequence as hereinabove described, as well as an appropriate promoter or control sequence, may be employed to transform an appropriate host to permit the host to express the protein.  
15

As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as *E. coli*, *Streptomyces*, *Bacillus subtilis*; fungal cells, such as yeast; insect cells such as *Drosophila S2* and *Spodoptera Sf9*; animal cells such as CHO, COS or Bowes melanoma; adenoviruses; plant cells, *etc.* The selection of an  
20 appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein.

More particularly, the present invention also includes recombinant constructs comprising one or more of the sequences as broadly described above. The constructs  
25 comprise a vector, such as a plasmid or viral vector, into which a sequence of the invention has been inserted, in a forward or reverse orientation. In a preferred aspect of this embodiment, the construct further comprises regulatory sequences, including, for example, a promoter, operably linked to the sequence. One or more additional inserts may also be incorporated that lead to expression of one or more additional molecules,  
30 such as another phytase or a protease enzyme, preferably said one or more additional molecules are serviceable in combination with the instant phytase in a combination treatment.

Large numbers of suitable vectors and promoters are known to those of skill in the art, and are commercially available. "Plasmids" are designated by a lower case p preceded and/or followed by capital letters and/or numbers. The starting plasmids herein are either commercially available, publicly available on an unrestricted basis, or  
5 can be constructed from available plasmids in accord with published procedures. In addition, equivalent plasmids to those described are known in the art and will be apparent to the ordinarily skilled artisan.

The following vectors are provided by way of example; Bacterial: pQE70,  
10 pQE60, pQE-9 (Qiagen), pBluescript II (Stratagene); pTRC99a, pKK223-3, pDR540, pRIT2T (Pharmacia); Eukaryotic: pXT1, pSG5 (Stratagene) pSVK3, pBPV, pMSG, pSVLSV40 (Pharmacia). However, any other plasmids or other vectors may be used as long as they are replicable and viable in the host.

15 Promoter regions can be selected from any desired gene using CAT (chloramphenicol transferase) vectors or other vectors with selectable markers. Two appropriate vectors are pKK232-8 and pCM7. Particular named bacterial promoters include lacI, lacZ, T3, T7, gpt, lambda P<sub>R</sub>, P<sub>L</sub> and trp. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from  
20 retrovirus, and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art.

In a further embodiment, the present invention relates to host cells containing the above-described constructs. The host cell can be a higher eukaryotic cell, such as a  
25 mammalian cell, or a lower eukaryotic cell, such as a yeast cell, or the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-Dextran mediated transfection, or electroporation (Davis, 1986).

30 The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Alternatively, the enzymes of the invention can be synthetically produced by conventional peptide synthesizers.

Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA constructs of the present invention. Appropriate cloning and expression vectors for use with  
5 prokaryotic and eukaryotic hosts are described (*e.g.* Sambrook *et al.*, 1989, the disclosure of which is hereby incorporated by reference).

Transcription of the DNA encoding the enzymes of the present invention by higher eukaryotes is increased by inserting an enhancer sequence into the vector.

10 Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp that act on a promoter to increase its transcription. Examples include the SV40 enhancer on the late side of the replication origin bp 100 to 270, a cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers.

15 Generally, recombinant expression vectors will include origins of replication and selectable markers permitting transformation of the host cell, *e.g.*, the ampicillin resistance gene of *E. coli* and *S. cerevisiae* TRP1 gene, and a promoter derived from a highly-expressed gene to direct transcription of a downstream structural sequence.

20 Such promoters can be derived from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK),  $\lambda$ -factor, acid phosphatase, or heat shock proteins, among others. The heterologous structural sequence is assembled in appropriate phase with translation initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated enzyme. Optionally, the heterologous  
25 sequence can encode a fusion enzyme including an N-terminal identification peptide imparting desired characteristics, *e.g.*, stabilization or simplified purification of expressed recombinant product.

Useful expression vectors for bacterial use are constructed by inserting a  
30 structural DNA sequence encoding a desired protein together with suitable translation initiation and termination signals in operable reading phase with a functional promoter. The vector will comprise one or more phenotypic selectable markers and an origin of replication to ensure maintenance of the vector and to, if desirable, provide

amplification within the host. Suitable prokaryotic hosts for transformation include *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium* and various species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*, although others may also be employed as a matter of choice.

5

As a representative but nonlimiting example, useful expression vectors for bacterial use can comprise a selectable marker and bacterial origin of replication derived from commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017). Such commercial vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and GEM1 (Promega Biotec, Madison, WI, USA). These pBR322 “backbone” sections are combined with an appropriate promoter and the structural sequence to be expressed.

10

Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter is induced by appropriate means (*e.g.*, temperature shift or chemical induction) and cells are cultured for an additional period.

15

Cells are typically harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract retained for further purification.

20

Microbial cells employed in expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents, such methods are well known to those skilled in the art.

25

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, as described (Gluzman, 1981), and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer, and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking nontranscribed sequences. DNA sequences derived from the

30



SV40 splice, and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

The enzyme can be recovered and purified from recombinant cell cultures by methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the mature protein. Finally, high performance liquid chromatography (HPLC) can be employed for final purification steps.

The enzymes of the present invention may be a naturally purified product, or a product of chemical synthetic procedures, or produced by recombinant techniques from a prokaryotic or eukaryotic host (for example, by bacterial, yeast, higher plant, insect and mammalian cells in culture). Depending upon the host employed in a recombinant production procedure, the enzymes of the present invention may be glycosylated or may be non-glycosylated. Enzymes of the invention may or may not also include an initial methionine amino acid residue.

In a preferred embodiment, the enzyme of the present invention is a phytase enzyme which is stable to heat and is heat resistant and catalyzes the enzymatic hydrolysis of phytate, *i.e.*, the enzyme is able to renature and regain activity after a brief (*i.e.*, 5 to 30 seconds), or longer period, for example, minutes or hours, exposure to temperatures of up to about 50 °C or slightly above 50 °C.

The present invention is further described with reference to the examples contained herein; however, it is to be understood that the present invention is not limited to such examples. All parts or amounts, unless otherwise specified, are by weight.

In one aspect of the invention, a method for producing an phytase enzyme, such as those shown in Figures 1, is provided. The method includes growing a host cell which contains a polynucleotide encoding the enzyme (*e.g.*, SEQ ID NO: 1), under

conditions which allow the expression of the nucleic acid, and optionally isolating the enzyme encoded by the nucleic acid. Methods of culturing the host cell are described in the Examples and are known by those of skill in the art.

5           **6.2.3 - Use of transgenic plants and plant organs:** In a particular embodiment, the present invention provides for the expression of phytase in transgenic plants or plant organs and methods for the production thereof. DNA expression constructs are provided for the transformation of plants with a gene encoding phytase under the control of regulatory sequences which are capable of directing the expression  
10 of phytase. These regulatory sequences include sequences capable of directing transcription in plants, either constitutively, or in stage and/or tissue specific manners.

The manner of expression depends, in part, on the use of the plant or parts thereof. The transgenic plants and plant organs provided by the present invention may  
15 be applied to a variety of industrial processes either directly, *e.g.* in animal feeds or alternatively, the expressed phytase may be extracted and if desired, purified before application. Alternatively, the recombinant host plant or plant part may be used directly. In a particular aspect, the present invention provides methods of catalyzing phytate-hydrolyzing reactions using seeds containing enhanced amounts of phytase.  
20 The method involves contacting transgenic, non-wild type seeds, preferably in a ground or chewed form, with phytate-containing substrate and allowing the enzymes in the seeds to increase the rate of reaction. By directly adding the seeds to a phytate-containing substrate, the invention provides a solution to the expensive and problematic process of extracting and purifying the enzyme. In a particular – but by no means  
25 limiting – exemplification, the present invention also provides methods of treatment whereby an organism lacking a sufficient supply of an enzyme is administered the enzyme in the form of seeds containing enhanced amounts of the enzyme. In a preferred embodiment, the timing of the administration of the enzyme to an organism is coordinated with the consumption of a phytate-containing foodstuff.

30           The expression of phytase in plants can be achieved by a variety of means. Specifically, for example, technologies are available for transforming a large number of plant species, including dicotyledonous species (*e.g.* tobacco, potato, tomato, Petunia,

Brassica). Additionally, for example, strategies for the expression of foreign genes in plants are available. Additionally still, regulatory sequences from plant genes have been identified that are serviceable for the construction of chimeric genes that can be functionally expressed in plants and in plant cells (*e.g.* Klee *et al.*, 1987; Clark *et al.*, 1990; Smith *et al.*, 1990).

The introduction of gene constructs into plants can be achieved using several technologies including transformation with *Agrobacterium tumefaciens* or *Agrobacterium rhizogenes*. Non-limiting examples of plant tissues that can be transformed thusly include protoplasts, microspores or pollen, and explants such as leaves, stems, roots, hypocotyls, and cotyls. Furthermore, DNA can be introduced directly into protoplasts and plant cells or tissues by microinjection, electroporation, particle bombardment, and direct DNA uptake.

Proteins may be produced in plants by a variety of expression systems. For instance, the use of a constitutive promoter such as the 35S promoter of Cauliflower Mosaic Virus (Guilley *et al.*, 1982) is serviceable for the accumulation of the expressed protein in virtually all organs of the transgenic plant. Alternatively, the use of promoters that are highly tissue-specific and/or stage-specific are serviceable for this invention (Higgins, 1984; Shotwell, 1989) in order to bias expression towards desired tissues and/or towards a desired stage of development. Further details relevant to the expression in plants of the phytase molecules of the instant invention are disclosed, for example, in USPN 5,770,413 (Van Ooijen *et al.*) and USPN 5,593,963 (Van Ooijen *et al.*), although these reference do not teach the inventive molecules of the instant application and instead teach the use of fungal phytases.

In sum, it is relevant to this invention that a variety of means can be used to achieve the recombinant expression of phytase in a transgenic plant or plant part. Such a transgenic plants and plant parts are serviceable as sources of recombinantly expressed phytase, which can be added directly to phytate-containing sources. Alternatively, the recombinant plant-expressed phytase can be extracted away from the plant source and, if desired, purified prior to contacting the phytase substrate.

#### 6.2.4 - Examples of serviceable plants:

Within the context of the present invention, plants to be selected include, but are not limited to crops producing edible flowers such as cauliflower (*Brassica oleracea*), artichoke (*Cynara scolymus*), fruits such as apple (*Malus, e.g. domestica*), banana (*Musa, e.g. acuminata*), berries (such as the currant, *Ribes, e.g. rubrum*), cherries (such as the sweet cherry, *Prunus, e.g. avium*), cucumber (*Cucumis, e.g. sativus*), grape (*Vitis, e.g. vinifera*), lemon (*Citrus limon*), melon (*Cucumis melo*), nuts (such as the walnut, *Juglans, e.g. regia*; peanut, *Arachis hypogaea*), orange (*Citrus, e.g. maxima*), peach (*Prunus, e.g. persica*), pear (*Pyra, e.g. communis*), plum (*Prunus, e.g. domestica*), strawberry (*Fragaria, e.g. moschata*), tomato (*Lycopersicon, e.g. esculentum*), leafs, such as alfalfa (*Medicago, e.g. sativa*), cabbages (*e.g. Brassica oleracea*), endive (*Cichoreum, e.g. endivia*), leek (*Allium, e.g. porrum*), lettuce (*Lactuca, e.g. sativa*), spinach (*Spinacia, e.g. oleraceae*), tobacco (*Nicotiana, e.g. tabacum*), roots, such as arrowroot (*Maranta, e.g. arundinacea*), beet (*Beta, e.g. vulgaris*), carrot (*Daucus, e.g. carota*), cassava (*Manihot, e.g. esculenta*), turnip (*Brassica, e.g. rapa*), radish (*Raphanus, e.g. sativus*), yam (*Dioscorea, e.g. esculenta*), sweet potato (*Ipomoea batatas*) and seeds, such as bean (*Phaseolus, e.g. vulgaris*), pea (*Pisum, e.g. sativum*), soybean (*Glycin, e.g. max*), wheat (*Triticum, e.g. aestivum*), barley (*Hordeum, e.g. vulgare*), corn (*Zea, e.g. mays*), rice (*Oryza, e.g. sativa*), rapeseed (*Brassica napus*), millet (*Panicum L.*), sunflower (*Helianthus annus*), oats (*Avena sativa*), tubers, such as kohlrabi (*Brassica, e.g. oleraceae*), potato (*Solanum, e.g. tuberosum*) and the like.

It is understood that additional plant as well as non-plant expression systems can be used within the context of this invention. The choice of the plant species is primarily determined by the intended use of the plant or parts thereof and the amenability of the plant species to transformation.

#### 6.2.5 - Plant transformation methods:

Several techniques are available for the introduction of the expression construct containing the phytase-encoding DNA sequence into the target plants. Such techniques include but are not limited to transformation of protoplasts using the calcium/polyethylene glycol method, electroporation and microinjection or (coated) particle bombardment (Potrykus, 1990). In addition to these so-called direct DNA transformation methods, transformation

systems involving vectors are widely available, such as viral vectors (*e.g.* from the Cauliflower Mosaic Virus (CaMV) and bacterial vectors (*e.g.* from the genus *Agrobacterium*) (Potrykus, 1990). After selection and/or screening, the protoplasts, cells or plant parts that have been transformed can be regenerated into whole plants, using methods known in the art (Horsch *et al.*, 1985). The choice of the transformation and/or regeneration techniques is not critical for this invention.

**6.2.6 - Methods for dicots:** For dicots, a preferred embodiment of the present invention uses the principle of the binary vector system (Hoekema *et al.*, 1983; EP 0120516 Schilperoort *et al.*) in which *Agrobacterium* strains are used which contain a vir plasmid with the virulence genes and a compatible plasmid containing the gene construct to be transferred. This vector can replicate in both *E. coli* and in *Agrobacterium*, and is derived from the binary vector Bin19 (Bevan, 1984) which is altered in details that are not relevant for this invention. The binary vectors as used in this example contain between the left- and right-border sequences of the T-DNA, an identical NPTII-gene coding for kanamycin resistance (Bevan, 1984) and a multiple cloning site to clone in the required gene constructs.

**6.2.7 - Methods for monocots:** The transformation and regeneration of monocotyledonous crops is not a standard procedure. However, recent scientific progress shows that in principle monocots are amenable to transformation and that fertile transgenic plants can be regenerated from transformed cells. The development of reproducible tissue culture systems for these crops, together with the powerful methods for introduction of genetic material into plant cells has facilitated transformation. Presently the methods of choice for transformation of monocots are microprojectile bombardment of explants or suspension cells, and direct DNA uptake or electroporation of protoplasts. For example, transgenic rice plants have been successfully obtained using the bacterial *hph* gene, encoding hygromycin resistance, as a selection marker. The gene was introduced by electroporation (Shimamoto *et al.*, 1993). Transgenic maize plants have been obtained by introducing the *Streptomyces hygrosopicus* *bar* gene, which encodes phosphinothricin acetyltransferase (an enzyme which inactivates the herbicide phosphinothricin), into embryogenic cells of a maize suspension culture by microparticle bombardment (Gordon-Kamm *et al.*, 1990). The introduction of

genetic material into aleurone protoplasts of other monocot crops such as wheat and barley has been reported (Lee *et al.*, 1989). Wheat plants have been regenerated from embryogenic suspension culture by selecting only the aged compact and nodular embryogenic callus tissues for the establishment of the embryogenic suspension cultures (Vasil *et al.*, 1972; Vasil *et al.*, 1974). The combination with transformation systems for these crops enables the application of the present invention to monocots. These methods may also be applied for the transformation and regeneration of dicots.

#### 6.2.8 - Methods for expression in plants: Expression of the phytase

construct involves such details as transcription of the gene by plant polymerases, translation of mRNA, etc. that are known to persons skilled in the art of recombinant DNA techniques. Only details relevant for the proper understanding of this invention are discussed below. Regulatory sequences which are known or are found to cause expression of phytase may be used in the present invention. The choice of the regulatory sequences used depends on the target crop and/or target organ of interest. Such regulatory sequences may be obtained from plants or plant viruses, or may be chemically synthesized. Such regulatory sequences are promoters active in directing transcription in plants, either constitutively or stage and/or tissue specific, depending on the use of the plant or parts thereof. These promoters include, but are not limited to promoters showing constitutive expression, such as the 35S promoter of Cauliflower Mosaic Virus (CaMV) (Guilley *et al.*, 1982), those for leaf-specific expression, such as the promoter of the ribulose biphosphate carboxylase small subunit gene (Coruzzi *et al.*, 1984), those for root-specific expression, such as the promoter from the glutamine synthase gene (Tingey *et al.*, 1987), those for seed-specific expression, such as the cruciferin A promoter from *Brassica napus* (Ryan *et al.*, 1989), those for tuber-specific expression, such as the class-I patatin promoter from potato (Koster-Topfer *et al.*, 1989; Wenzler *et al.*, 1989) or those for fruit-specific expression, such as the polygalacturonase (PG) promoter from tomato (Bird *et al.*, 1988).

Other regulatory sequences such as terminator sequences and polyadenylation signals include any such sequence functioning as such in plants, the choice of which is within the level of the skilled artisan. An example of such sequences is the 3' flanking region of the nopaline synthase (nos) gene of *Agrobacterium tumefaciens* (Bevan,

*supra*). The regulatory sequences may also include enhancer sequences, such as found in the 35S promoter of CaMV, and mRNA stabilizing sequences such as the leader sequence of Alfalfa Mosaic Virus (AIMV) RNA4 (Brederode *et al.*, 1980) or any other sequences functioning in a like manner.

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The phytase should be expressed in an environment that allows for stability of the expressed protein. The choice of cellular compartments, such as cytosol, endoplasmic reticulum, vacuole, protein body or periplasmic space can be used in the present invention to create such a stable environment, depending on the biophysical parameters of the phytase. Such parameters include, but are not limited to pH-  
10 optimum, sensitivity to proteases or sensitivity to the molarity of the preferred compartment.

To obtain expression in the cytoplasm of the cell, the expressed enzyme should  
15 not contain a secretory signal peptide or any other target sequence. For expression in chloroplasts and mitochondria the expressed enzyme should contain specific so-called transit peptide for import into these organelles. Targeting sequences that can be attached to the enzyme of interest in order to achieve this are known (Smeekens *et al.*, 1990; van den Broeck *et al.*, 1985; Wolter *et al.*, 1988). If the activity of the enzyme is  
20 desired in the vacuoles a secretory signal peptide has to be present, as well as a specific targeting sequence that directs the enzyme to these vacuoles (Tague *et al.*, 1990). The same is true for the protein bodies in seeds. The DNA sequence encoding the enzyme of interest should be modified in such a way that the enzyme can exert its action at the desired location in the cell.

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To achieve extracellular expression of the phytase, the expression construct of the present invention utilizes a secretory signal sequence. Although signal sequences which are homologous (native) to the plant host species are preferred, heterologous signal sequences, *i.e.* those originating from other plant species or of microbial origin,  
30 may be used as well. Such signal sequences are known to those skilled in the art. Appropriate signal sequences which may be used within the context of the present invention are disclosed in Blobel *et al.*, 1979; Von Heijne, 1986; Garcia *et al.*, 1987; Sijmons *et al.*, 1990; Ng *et al.*, 1994; and Powers *et al.*, 1996).

All parts of the relevant DNA constructs (promoters, regulatory-, secretory-, stabilizing-, targeting-, or termination sequences) of the present invention may be modified, if desired, to affect their control characteristics using methods known to those skilled in the art. It is pointed out that plants containing phytase obtained via the present invention may be used to obtain plants or plant organs with yet higher phytase levels. For example, it may be possible to obtain such plants or plant organs by the use of somoclonal variation techniques or by cross breeding techniques. Such techniques are well known to those skilled in the art.

#### 6.2.9 - Dual expression of novel phytase & other molecules:

In one embodiment, the instant invention provides a method (and products thereof) of achieving a highly efficient overexpression system for phytase and other molecules. In a preferred embodiment, the instant invention provides a method (and products thereof) of achieving a highly efficient overexpression system for phytase and pH 2.5 acid phosphatase in *Trichoderma*. This system results in enzyme compositions that have particular utility in the animal feed industry. Additional details regarding this approach are in the public literature and/or are known to the skilled artisan. In a particular non-limiting exemplification, such publicly available literature includes EP 0659215 (W0 9403612 A1) (Nevalainen *et al.*), although these reference do not teach the inventive molecules of the instant application.

#### 6.2.10 - Soluble preparation of novel phytase & stabilized liquid

**formulations thereof:** In one embodiment, the instant invention provides a method (and products thereof) of producing stabilized aqueous liquid formulations having phytase activity that exhibit increased resistance to heat inactivation of the enzyme activity and which retain their phytase activity during prolonged periods of storage. The liquid formulations are stabilized by means of the addition of urea and/or a polyol such as sorbitol and glycerol as stabilizing agent. Also provided are feed preparations for monogastric animals and methods for the production thereof that result from the use of such stabilized aqueous liquid formulations. Additional details regarding this approach are in the public literature and/or are known to the skilled artisan. In a particular non-limiting exemplification, such publicly available literature includes EP 0626010 (W0



9316175 A1) (Barendse *et al.*), although references in the publicly available literature do not teach the inventive molecules of the instant application.

### 6.3 - Use of Novel Phytase

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6.3.1 - **General uses, hydrolysis of phytate, & generation of inositol:** In one embodiment, the instant invention provides a method of hydrolyzing phytate comprised of contacting the phytate with one or more of the novel phytase molecules disclosed herein. Accordingly, the invention provides a method for catalyzing the hydrolysis of  
10 phytate to inositol and free phosphate with release of minerals from the phytic acid complex. The method includes contacting a phytate substrate with a degrading effective amount of an enzyme of the invention, such as the enzyme shown in SEQ ID NO:2. The term “degrading effective” amount refers to the amount of enzyme which is required to degrade at least 50% of the phytate, as compared to phytate not contacted  
15 with the enzyme. Preferably, at least 80% of the phytate is degraded.

In another embodiment, the invention provides a method for hydrolyzing phospho-mono-ester bonds in phytate. The method includes administering an effective amount of phytase molecules of the invention (*e.g.*, SEQ ID NO:2), to yield inositol  
20 and free phosphate. An “effective” amount refers to the amount of enzyme which is required to hydrolyze at least 50% of the phospho-mono-ester bonds, as compared to phytate not contacted with the enzyme. Preferably, at least 80% of the bonds are hydrolyzed.

25 In a particular aspect, when desired, the phytase molecules may be used in combination with other reagents, such as other catalysts; in order to effect chemical changes (*e.g.* hydrolysis) in the phytate molecules and/or in other molecules of the substrate source(s). According to this aspect, preferably the phytase molecules and the additional reagent(s) will not inhibit each other, more preferably the phytase molecules  
30 and the additional reagent(s) will have an overall additive effect, and more preferably still the phytase molecules and the additional reagent(s) will have an overall synergistic effect.

Relevant sources of the substrate phytate molecules include foodstuffs, potential foodstuffs, byproducts of foodstuffs (both *in vitro* byproducts and *in vivo* byproducts, *e.g.* ex vivo reaction products and animal excremental products), precursors of foodstuffs, and any other material source of phytate.

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**6.3.2 - Administration to organisms:** In a non-limiting aspect, the recombinant phytase can be consumed by organisms and retains activity upon consumption. In another exemplification, transgenic approaches can be used to achieve expression of the recombinant phytase – preferably in a controlled fashion (methods are available for controlling expression of transgenic molecules in time-specific and tissue specific manners).

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In a particular exemplification, the phytase activity in the source material (*e.g.* a transgenic plant source or a recombinant prokaryotic host) may be increased upon consumption; this increase in activity may occur, for example, upon conversion of a precursor phytase molecule in pro-form to a significantly more active enzyme in a more mature form, where said conversion may result, for example, from the injection and digestion of the phytase source. Hydrolysis of the phytate substrate may occur at any time upon the contacting of the phytase with the phytate; for example, this may occur before injection or after injection or both before and after injection of either the substrate or the enzyme or both. It is additionally appreciated that the phytate substrate may be contacted with – in addition to the phytase – one or more additional reagents, such as another enzyme, which may be also be applied either directly or after purification from its source material.

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It is appreciated that the phytase source material(s) can be contacted directly with the phytate source material(s); *e.g.* upon *in vitro* or *in vivo* grinding or chewing of either or both the phytase source(s) and the phytate source(s). Alternatively the phytase enzyme may be purified away from source material(s), or the phytate substrate may be purified away from source material(s), or both the phytase enzyme and the phytate substrate may be purified away from source material(s) prior to the contacting of the phytase enzyme with the phytate substrate. It is appreciated that a combination of

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purified and unpurified reagents - including enzyme(s) or substrates(s) or both – may be used.

It is appreciated that more than one source material may be used as a source of phytase activity. This is serviceable as one way to achieve a timed release of reagent(s) from source material(s), where release from different reagents from their source materials occur differentially, for example as injected source materials are digested *in vivo* or as source materials are processed in *in vitro* applications. The use of more than one source material of phytase activity is also serviceable to obtain phytase activities under a range of conditions and fluctuations thereof, that may be encountered - such as a range of pH values, temperatures, salinities, and time intervals – for example during different processing steps of an application. The use of different source materials is also serviceable in order to obtain different reagents, as exemplified by one or more forms or isomers of phytase and/or phytate &/or other materials.

It is appreciated that a single source material, such a transgenic plant species (or plant parts thereof), may be a source material of both phytase and phytate; and that enzymes and substrates may be differentially compartmentalized within said single source – *e.g.* secreted vs. non-secreted, differentially expressed &/or having differential abundances in different plant parts or organs or tissues or in subcellular compartments within the same plant part or organ or tissue. Purification of the phytase molecules contained therein may comprise isolating and/or further processing of one or more desirable plant parts or organs or tissues or subcellular compartments.

In a particular aspect, this invention provides a method of catalyzing *in vivo* and/or *in vitro* reactions using seeds containing enhanced amounts of enzymes. The method comprises adding transgenic, non-wild type seeds, preferably in a ground form, to a reaction mixture and allowing the enzymes in the seeds to increase the rate of reaction. By directly adding the seeds to the reaction mixture the method provides a solution to the more expensive and cumbersome process of extracting and purifying the enzyme. Methods of treatment are also provided whereby an organism lacking a sufficient supply of an enzyme is administered the enzyme in the form of seeds from one or more plant species, preferably transgenic plant species, containing enhanced

amounts of the enzyme. Additional details regarding this approach are in the public literature and/or are known to the skilled artisan. In a particular non-limiting exemplification, such publicly available literature includes USPN 5,543,576 (Van Ooijen *et al.*) and USPN 5,714,474 (Van Ooijen *et al.*), although these reference do not teach the inventive molecules of the instant application and instead teach the use of fungal phytases.

In a particular non-limiting aspect, the instant phytase molecules are serviceable for generating recombinant digestive system life forms (or microbes or flora) and for the administration of said recombinant digestive system life forms to animals. Administration may be optionally performed alone or in combination with other enzymes &/or with other life forms that can provide enzymatic activity in a digestive system, where said other enzymes and said life forms may be may recombinant or otherwise. For example, administration may be performed in combination with xylanolytic bacteria

**6.3.3 - Steeping of cereals:** In a non-limiting aspect, the present invention provides a method for steeping corn or sorghum kernels in warm water containing sulfur dioxide in the presence of an enzyme preparation comprising one or more phytin-degrading enzymes, preferably in such an amount that the phytin present in the corn or sorghum is substantially degraded. The enzyme preparation may comprise phytase and/or acid phosphatase and optionally other plant material degrading enzymes. The steeping time may be 12 to 18 hours. The steeping may be interrupted by an intermediate milling step, reducing the steeping time. In a preferred embodiment, corn or sorghum kernels are steeped in warm water containing sulfur dioxide in the presence of an enzyme preparation including one or more phytin-degrading enzymes, such as phytase and acid phosphatases, to eliminate or greatly reduce phytic acid and the salts of phytic acid. Additional details regarding this approach are in the public literature and/or are known to the skilled artisan. In a particular non-limiting exemplification, such publicly available literature includes USPN 4,914,029 (Caransa *et al.*) and EP 0321004 (Vaara *et al.*), although these reference do not teach the inventive molecules of the instant application.

**6.3.4 - Preparation of bread dough:** In a non-limiting aspect, the present invention provides a method to obtain a bread dough having desirable physical properties such as non-tackiness and elasticity and a bread product of superior quality such as a specific volume comprising adding phytase molecules to the bread dough. In a preferred embodiment, phytase molecules of the instant invention are added to a working bread dough preparation that is subsequently formed and baked. Additional details regarding this approach are in the public literature and/or are known to the skilled artisan. In a particular non-limiting exemplification, such publicly available literature includes JP 03076529 (Hara *et al.*), although this reference does not teach the inventive phytase molecules of the instant application.

**6.3.5 - Production of soybean-containing foodstuffs:** In a non-limiting aspect, the present invention provides a method to produce improved soybean foodstuffs. Soybeans are combined with phytase molecules of the instant invention to remove phytic acid from the soybeans, thus producing soybean foodstuffs that are improved in their supply of trace nutrients essential for consuming organisms and in its digestibility of proteins. In a preferred embodiment, in the production of soybean milk, phytase molecules of the instant invention are added to or brought into contact with soybeans in order to reduce the phytic acid content. In a non-limiting exemplification, the application process can be accelerated by agitating the soybean milk together with the enzyme under heating or by a conducting a mixing-type reaction in an agitation container using an immobilized enzyme. Additional details regarding this approach are in the public literature and/or are known to the skilled artisan. In a particular non-limiting exemplification, such publicly available literature includes JP 59166049 (Kamikubo *et al.*), although this reference does not teach the inventive molecules of the instant application.

**6.3.6 - Production of liquid foodstuffs including sake:** In one aspect, the instant invention provides a method of producing an admixture product for drinking water or animal feed in fluid form, and which comprises using mineral mixtures and vitamin mixtures, and also novel phytase molecules of the instant invention. In a preferred embodiment, there is achieved a correctly dosed and composed mixture of

necessary nutrients for the consuming organism without any risk of precipitation and destruction of important minerals/vitamins, while at the same time optimum utilization is made of the phytin-bound phosphate in the feed. Additional details regarding this approach are in the public literature and/or are known to the skilled artisan. In a particular non-limiting exemplification, such publicly available literature includes EP 0772978 (Bendixen *et al.*), although this reference does not teach the inventive molecules of the instant application.

It is appreciated that the phytase molecules of the instant invention may also be used to produce other alcoholic and non-alcoholic drinkable foodstuffs (or drinks) based on the use of molds &/or on grains &/or on other plants. These drinkable foodstuffs include liquors, wines, mixed alcoholic drinks (*e.g.* wine coolers, other alcoholic coffees such as Irish coffees, etc.), beers, near-beers, juices, extracts, homogenates, and purees. In a preferred exemplification, the instantly disclosed phytase molecules are used to generate transgenic versions of molds &/or grains &/or other plants serviceable for the production of such drinkable foodstuffs. In another preferred exemplification, the instantly disclosed phytase molecules are used as additional ingredients in the manufacturing process &/or in the final content of such drinkable foodstuffs. Additional details regarding this approach are in the public literature and/or are known to the skilled artisan. However - due to the novelty of the instant invention - references in the publicly available literature do not teach the inventive molecules instantly disclosed.

In another non-limiting exemplification, the present invention provides a means to obtain refined sake having a reduced amount of phytin and an increased content of inositol. Such a sake may have – through direct &/or psychogenic effects - a preventive action on hepatic disease, arteriosclerosis, and other diseases. In a preferred embodiment, a sake is produced from rice Koji by multiplying a rice Koji mold having high phytase activity as a raw material. It is appreciated that the phytase molecules of the instant invention may be used to produce a serviceable mold with enhanced activity (preferably a transgenic mold) &/or added exogenously to augment the effects of a Koji mold. The strain is added to boiled rice and Koji is produced by a conventional procedure. In a preferred exemplification, the prepared Koji is used, the whole rice is

prepared at two stages and Sake is produced at constant Sake temperature of 15°C to give the objective refined Sake having a reduced amount of phytin and an increased amount of inositol. Additional details regarding this approach are in the public literature and/or are known to the skilled artisan. In a particular non-limiting exemplification, such publicly available literature includes JP 06153896 (Soga *et al.*) and JP 06070749 (Soga *et al.*), although these references do not teach the inventive molecules of the instant application

**6.3.7 - Production of mineral absorbefacient:** In a non-limiting aspect, the present invention provides a method to obtain an absorbefacient capable of promoting the absorption of minerals including ingested calcium without being digested by gastric juices or intestinal juices at a low cost. In a preferred embodiment, said mineral absorbefacient contains a partial hydrolysate of phytic acid as an active ingredient. Preferably, a partial hydrolyzate of the phytic acid is produced by hydrolyzing the phytic acid or its salts using novel phytase molecules of the instant invention. The treatment with said phytase molecules may occur either alone &/or in a combination treatment (to inhibit or to augment the final effect), and is followed by inhibiting the hydrolysis within a range so as not to liberate all the phosphate radicals. Additional details regarding this approach are in the public literature and/or are known to the skilled artisan. In a particular non-limiting exemplification, such publicly available literature includes JP 04270296 (Hoshino), although reference in the publicly available literature do not teach the inventive molecules of the instant application.

**6.3.8 - Use in combination with other phytases &/or acid phosphatases:** In a non-limiting aspect, the present invention provides a method (and products therefrom) to produce an enzyme composition having an additive or preferably a synergistic phytate hydrolyzing activity; said composition comprises novel phytase molecules of the instant invention and one or more additional reagents to achieve a composition that is serviceable for a combination treatment. In a preferred embodiment, the combination treatment of the present invention is achieved with the use of at least two phytases of different position specificity, *i.e.* any combinations of 1-, 2-, 3-, 4-, 5-, and 6-phytases. By combining phytases of different position specificity an additive or synergistic effect is obtained. Compositions such as food and feed or food and feed additives comprising

such phytases in combination are also included in this invention as are processes for their preparation. Additional details regarding this approach are in the public literature and/or are known to the skilled artisan. In a particular non-limiting exemplification, such publicly available literature includes WO9 830681 (Ohmann *et al.*), although  
5 references in the publicly available literature do not teach the use of the inventive molecules of the instant application.

In another preferred embodiment, the combination treatment of the present invention is achieved with the use of an acid phosphatase having phytate hydrolyzing  
10 activity at a pH of 2.5, in a low ratio corresponding to a pH 2.5:5.0 activity profile of from about 0.1:1.0 to 10:1, preferably of from about 0.5:1.0 to 5:1, more preferably still of from about 0.8:1.0 to 3:1, and more preferably still of from about 0.8:1.0 to 2:1. Said enzyme composition preferably displays a higher synergetic phytate hydrolyzing efficiency through thermal treatment. Said enzyme composition is serviceable in the  
15 treatment of foodstuffs (drinkable and solid food, feed and fodder products) to improve phytate hydrolysis. Additional details regarding this approach are in the public literature and/or are known to the skilled artisan. In a particular non-limiting exemplification, such publicly available literature includes USPN 5,554,399 (Vanderbeke *et al.*) and USPN 5,443,979 (Vanderbeke *et al.*), although these reference  
20 do not teach the use of the inventive molecules of the instant application, but rather teach the use of fungal (in particular *Aspegillus*) phytases.

**6.3.9 - Use in combination with enzymes that act on polysaccharides (e.g. xylanases):** In a non-limiting aspect, the present invention provides a method (and  
25 products therefrom) to produce composition comprised of the instant novel phytate-acting enzyme in combination with one or more additional enzymes that act on polysaccharides. Such polysaccharides can be selected from the group consisting of arabinans, fructans, fucans, galactans, galacturonans, glucans, mannans, xylans, levan, fucoidan, carrageenan, galactocarlose, pectin, pectic acid, amylose, pullulan,  
30 glycogen, amylopectin, cellulose, carboxymethylcellulose, hydroxypropylmethylcellulose, dextran, pustulan, chitin, agarose, keratan, chondroitin, dermatan, hyaluronic acid, alginic acid, and polysaccharides containing at least one aldose, ketose, acid or amine selected from the group consisting of erythrose, threose,



ribose, arabinose, xylose, lyxose, allose, altrose, glucose, mannose, gulose, idose, galactose, talose, erythrulose, ribulose, xylulose, psicose, fructose, sorbose, tagatose, glucuronic acid, gluconic acid, glucaric acid, galacturonic acid, mannuronic acid, glucosamine, galactosamine and neuraminic acid

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In a particular aspect, the present invention provides a method (and products therefrom) to produce composition having a synergistic phytate hydrolyzing activity comprising one or more novel phytase molecules of the instant invention, a cellulase (including preferably but not exclusively a xylanase), optionally a protease, and  
10 optionally one or more additional reagents. In preferred embodiments, such combination treatments are serviceable in the treatment of foodstuffs, wood products, such as paper products, and as cleansing solutions and solids.

In one non-limiting exemplification, the instant phytase molecules are  
15 serviceable in combination with cellulosome components. It is known that cellulases of many cellulolytic bacteria are organized into discrete multienzyme complexes, called cellulosomes. The multiple subunits of cellulosomes are composed of numerous functional domains, which interact with each other and with the cellulosic substrate. One of these subunits comprises a distinctive new class of noncatalytic scaffolding  
20 polypeptide, which selectively integrates the various cellulase and xylanase subunits into the cohesive complex. Intelligent application of cellulosome hybrids and chimeric constructs of cellulosomal domains should enable better use of cellulosic biomass and may offer a wide range of novel applications in research, medicine and industry.

In another non-limiting exemplification, the instant phytase molecules are  
25 serviceable - either alone or in combination treatments - in areas of biopulping and biobleaching where a reduction in the use of environmentally harmful chemicals traditionally used in the pulp and paper industry is desired. Waste water treatment represents another vast application area where biological enzymes have been shown to  
30 be effective not only in colour removal but also in the bioconversion of potentially noxious substances into useful bioproducts.

In another non-limiting exemplification, the instant phytase molecules are serviceable for generating life forms that can provide at least one enzymatic activity - either alone or in combination treatments - in the treatment of digestive systems of organisms. Particularly relevant organisms to be treated include non-ruminant organisms. Specifically, it is appreciated that this approach may be performed alone or in combination with other biological molecules (for example, xylanases) to generate a recombinant host that expresses a plurality of biological molecules. It is also appreciated that the administration of the instant phytase molecules &/or recombinant hosts expressing the instant phytase molecules may be performed either alone or in combination with other biological molecules, &/or life forms that can provide enzymatic activities in a digestive system - where said other enzymes and said life forms may be recombinant or otherwise. For example, administration may be performed in combination with xylanolytic bacteria

For example, in addition to phytate, many organisms are also unable to adequately digest hemicelluloses. Hemicelluloses or xylans are major components (35%) of plant materials. For ruminant animals, about 50% of the dietary xylans are degraded, but only small amounts of xylans are degraded in the lower gut of nonruminant animals and humans. In the rumen, the major xylanolytic species are *Butyrivibrio fibrisolvens* and *Bacteroides ruminicola*. In the human colon, *Bacteroides ovatus* and *Bacteroides fragilis* subspecies "a" are major xylanolytic bacteria. Xylans are chemically complex, and their degradation requires multiple enzymes. Expression of these enzymes by gut bacteria varies greatly among species. *Butyrivibrio fibrisolvens* makes extracellular xylanases but *Bacteroides* species have cell-bound xylanase activity. Biochemical characterization of xylanolytic enzymes from gut bacteria has not been done completely. A xylosidase gene has been cloned from *B. fibrisolvens* 113. The data from DNA hybridizations using a xylanase gene cloned from *B. fibrisolvens* 49 indicate this gene may be present in other *B. fibrisolvens* strains. A cloned xylanase from *Bact. ruminicola* was transferred to and highly expressed in *Bact. fragilis* and *Bact. uniformis*. Arabinosidase and xylosidase genes from *Bact. ovatus* have been cloned and both activities appear to be catalyzed by a single, bifunctional, novel enzyme.

Accordingly, it is appreciated that the present phytase molecules are serviceable for 1) transferring into a suitable host (such as *Bact. fragilis* or *Bact. uniformis*); 2) achieving adequate expression in a resultant recombinant host; and 3) administering said recombinant host to organisms to improve the ability of the treated organisms to  
5 degrade phytate. Continued research in genetic and biochemical areas will provide knowledge and insights for manipulation of digestion at the gut level and improved understanding of colonic fiber digestion.

Additional details regarding this approach are in the public literature and/or are  
10 known to the skilled artisan. In a particular non-limiting exemplification, such publicly available literature includes USPN 5,624,678 (Bedford *et al.*), USPN 5,683,911 (Bodie *et al.*), USPN 5,720,971 (Beauchemin *et al.*), USPN 5,759,840 (Sung *et al.*), USPN 5,770,012 (Cooper), USPN 5,786,316 (Baeck *et al.*), USPN 5,817,500 (Hansen *et al.*), and journal articles (Jeffries, 1996; Prade, 1996; Bayer *et al.*, 1994; Duarte *et al.*, 1994; Hespell & Whitehead, 1990; Wong *et al.*, 1988), although these reference do not teach  
15 the inventive phytase molecules of the instant application, nor do they all teach the addition of phytase molecules in the production of foodstuffs, wood products, such as paper products, and as cleansing solutions and solids. In contrast, the instant invention teaches that phytase molecules – preferably the inventive phytase molecules of the  
20 instant application - may be added to the reagent(s) disclosed in order to obtain preparations having an additional phytase activity. Preferably, said reagent(s) the additional phytase molecules and will not inhibit each other, more preferably said reagent(s) the additional phytase molecules will have an overall additive effect, and more preferably still said reagent(s) the additional phytase molecules will have an  
25 overall synergistic effect.

**6.3.10 - Use in combination with vitamin D:** In a non-limiting aspect, the present invention provides a method (and products therefrom) for enhancement of phytate phosphorus utilization and treatment and prevention of tibial dyschondroplasia  
30 in animals, particularly poultry, by administering to animals a feed composition containing a hydroxylated vitamin D<sub>3</sub> derivative. The vitamin D<sub>3</sub> derivative is preferably administered to animals in feed containing reduced levels of calcium and phosphorus for enhancement of phytate phosphorus utilization. Accordingly, the

vitamin D<sub>3</sub> derivative is preferably administered in combination with novel phytase molecules of the instant invention for further enhancement of phytate phosphorus utilization. Additional details regarding this approach are in the public literature and/or are known to the skilled artisan. In a particular non-limiting exemplification, such

5 publicly available literature includes USPN 5,516,525 (Edwards *et al.*) and USPN 5,366,736 (Edwards *et al.*), USPN 5,316,770 (Edwards *et al.*) although these reference do not teach the inventive molecules of the instant application.

**6.3.11 - Use in combination with lactic acid-producing bacteria:** In a non-

10 limiting aspect, the present invention provides a method (and products therefrom) to obtain foodstuff that 1) comprises phytin that is easily absorbed and utilized in a form of inositol in a body of an organism; 2) that is capable of reducing phosphorus in excrementary matter; and 3) that is accordingly useful for improving environmental pollution. Said foodstuff is comprised of an admixture of a phytin-containing grain, a

15 lactic acid-producing microorganism, and a novel phytase molecule of the instant invention. In a preferred embodiment, said foodstuff is produced by compounding a phytin- containing grain (preferably, *e.g.* rice bran) with an effective microbial group having an acidophilic property, producing lactic acid, without producing butyric acid, free from pathogenicity, and a phytase. Examples of an effective microbial group

20 include *e.g.* *Streptomyces sp.* (ATCC 3004) belonging to the group of actinomyces and *Lactobacillus sp.* (IFO 3070) belonging to the group of lactobacilli. Further, a preferable amount of addition of an effective microbial group is 0.2 wt. % in terms of bacterial body weight based on a grain material. Furthermore, the amount of the addition of the phytase is preferably 1-2 wt. % based on the phytin in the grain material.

25 Additional details regarding this approach are in the public literature and/or are known to the skilled artisan. In a particular non-limiting exemplification, such publicly available literature includes JP 08205785 (Akahori *et al.*), although references in the publicly available literature do not teach the inventive molecules of the instant application.

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**6.3.12 - Solubilization of proteins in combination with proteases:** In a non-limiting aspect, the present invention provides a method for improving the solubility of vegetable proteins. More specifically, the invention relates to methods for the

solubilization of proteins in vegetable protein sources, which methods comprise treating the vegetable protein source with an efficient amount of one or more phytase enzymes – including phytase molecules of the instant invention - and treating the vegetable protein source with an efficient amount of one or more proteolytic enzymes. In another aspect, the invention provides animal feed additives comprising a phytase and one or more proteolytic enzymes. Additional details regarding this approach are in the public literature and/or are known to the skilled artisan. In a particular non-limiting exemplification, such publicly available literature includes EP 0756457 (WO 9528850 A1) (Nielsen and Knap), although references in the publicly available literature do not teach the inventive molecules of the instant application.

In a non-limiting aspect, the present invention provides a method of producing a plant protein preparation comprising dispersing vegetable protein source materials in water at a pH in the range of 2 to 6 and admixing phytase molecules of the instant invention therein. The acidic extract containing soluble protein is separated and dried to yield a solid protein of desirable character. One or more proteases can also be used to improve the characteristics of the protein. Additional details regarding this approach are in the public literature and/or are known to the skilled artisan. In a particular non-limiting exemplification, such publicly available literature includes USPN 3,966,971 (Morehouse *et al.*), although references in the publicly available literature do not teach the inventive molecules of the instant application.

**6.3.13 - Triple treatment of compost using novel phytase, saponin, and chitosan:** In a non-limiting aspect, the present invention provides a method (and products thereof) to activate inert phosphorus in soil and/or compost, to improve the utilization rate of a nitrogen compound, and to suppress propagation of pathogenic molds by adding three reagents, phytase, saponin and chitosan, to the compost. In a non-limiting embodiment the method can comprise treating the compost by 1) adding phytase-containing microorganisms in media – preferably recombinant hosts that overexpress the novel phytase molecules of the instant invention - *e.g.* at 100 ml media/100 kg wet compost; 2) alternatively also adding a phytase-containing plant source - such as wheat bran - *e.g.* at 0.2 to 1 kg/100 kg wet compost; 3) adding a saponin-containing source - such as peat, mugworts and yucca plants – *e.g.* at 0.5 to

3.0g/kg ; 4) adding chitosan-containing materials – such as pulverized shells of shrimps, crabs, etc. – *e.g.* at 100 to 300g/kg wet compost. In another non-limiting embodiment, recombinant sources the three reagents, phytase, saponin, and chitosan, are used. Additional details regarding this approach are in the public literature and/or are known to the skilled artisan. In a particular non-limiting exemplification, such publicly available literature includes JP 07277865 (Toya Taisuke), although references in the publicly available literature do not teach the inventive molecules of the instant application.

**6.3.14 - Use as hybridization probes & amplification templates:** Fragments of the full length gene of the present invention may be used as a hybridization probe for a cDNA or a genomic library to isolate the full length DNA and to isolate other DNAs which have a high sequence similarity to the gene or similar biological activity. Probes of this type have at least 10, preferably at least 15, and even more preferably at least 30 bases and may contain, for example, at least 50 or more bases. The probe may also be used to identify a DNA clone corresponding to a full length transcript and a genomic clone or clones that contain the complete gene including regulatory and promotor regions, exons, and introns.

The present invention provides methods for identifying nucleic acid molecules that encode members of the phytase polypeptide family in addition to SEQ ID NO:1. In these methods, a sample, *e.g.*, a nucleic acid library, such as a cDNA library, that contains a nucleic acid encoding a phytase polypeptide is screened with a phytase-specific probe, *e.g.*, a phytase-specific nucleic acid probe. Phytase-specific nucleic acid probes are nucleic acid molecules (*e.g.*, molecules containing DNA or RNA nucleotides, or combinations or modifications thereof) that specifically hybridize to nucleic acids encoding phytase polypeptides, or to complementary sequences thereof. The term “phytase-specific probe,” in the context of this method of invention, refers to probes that bind to nucleic acids encoding phytase polypeptides, or to complementary sequences thereof, to a detectably greater extent than to nucleic acids encoding other enzymes, or to complementary sequences thereof.

The invention facilitates production of phytase-specific nucleic acid probes. Methods for obtaining such probes can be designed based on the amino acid sequences shown in Figure 1. The probes, which can contain at least 12, *e.g.*, at least 15, 25, 35, 50, 100, or 150 nucleotides, can be produced using any of several standard methods (see, *e.g.*, Ausubel *et al.*, *supra*). For example, preferably, the probes are generated using PCR amplification methods. In these methods, primers are designed that correspond to phytase-conserved sequences (see Figure 1), which can include phytase-specific amino acids, and the resulting PCR product is used as a probe to screen a nucleic acid library, such as a cDNA library.

This invention can be used to isolate nucleic acid sequences substantially similar to the isolated nucleic acid molecule encoding an phytase enzyme disclosed in Figure 1 (SEQ ID NO:1). Isolated nucleic acid sequences are substantially similar if: (i) they are capable of hybridizing under stringent conditions, hereinafter described, to SEQ ID NO:1; or (ii) they encode a phytase polypeptide as set forth in SEQ ID NO:2 due to the degeneracy of the genetic code (*e.g.*, degenerate to SEQ ID NO:1).

Degenerate DNA sequences encode the amino acid sequence of SEQ ID NO:2, but have variations in the nucleotide coding sequences. As used herein, "substantially similar" refers to the sequences having similar identity to the sequences of the instant invention. The nucleotide sequences that are substantially similar can be identified by hybridization or by sequence comparison. Enzyme sequences that are substantially similar can be identified by one or more of the following: proteolytic digestion, gel electrophoresis and/or microsequencing.

One means for isolating a nucleic acid molecule encoding a phytase enzyme is to probe a genomic gene library with a natural or artificially designed probe using art recognized procedures (see, *e.g.*, Ausubel *et al.*, *supra*). It is appreciated to one skilled in the art that SEQ ID NO:1, or fragments thereof (comprising at least 15 contiguous nucleotides), is a particularly useful probe. Other particular useful probes for this purpose are hybridizable fragments to the sequences of SEQ ID NO:1 (*i.e.*, comprising at least 15 contiguous nucleotides).

It is also appreciated that such probes can be and are preferably labeled with an analytically detectable reagent to facilitate identification of the probe. Useful reagents include but are not limited to radioactivity, fluorescent dyes or enzymes capable of catalyzing the formation of a detectable product. The probes are thus useful to isolate complementary copies of DNA from other animal sources or to screen such sources for related sequences.

With respect to nucleic acid sequences which hybridize to specific nucleic acid sequences disclosed herein, hybridization may be carried out under conditions of reduced stringency, medium stringency or even stringent conditions. As an example of oligonucleotide hybridization, a polymer membrane containing immobilized denatured nucleic acid is first prehybridized for 30 minutes at 45°C in a solution consisting of 0.9 M NaCl, 50 mM NaH<sub>2</sub>PO<sub>4</sub>, pH 7.0, 5.0 mM Na<sub>2</sub>EDTA, 0.5% SDS, 10X Denhardt's, and 0.5 mg/mL polyriboadenylic acid. Approximately 2 X 10<sup>7</sup> cpm (specific activity 4-9 X 10<sup>8</sup> cpm/ug) of <sup>32</sup>P end-labeled oligonucleotide probe are then added to the solution. After 12-16 hours of incubation, the membrane is washed for 30 minutes at room temperature in 1X SET (150 mM NaCl, 20 mM Tris hydrochloride, pH 7.8, 1 mM Na<sub>2</sub>EDTA) containing 0.5% SDS, followed by a 30 minute wash in fresh 1X SET at Tm-10°C for the oligo-nucleotide probe. The membrane is then exposed to autoradiographic film for detection of hybridization signals.

The nucleic acid molecules of the invention can be used as templates in standard methods for production of phytase gene products (*e.g.*, phytase RNAs and phytase polypeptides). In addition, the nucleic acid molecules that encode phytase polypeptides (and fragments thereof) and related nucleic acids - such as (1) nucleic acids containing sequences that are complementary to, or that hybridize to, nucleic acids encoding phytase polypeptides, or fragments thereof (*e.g.*, fragments containing at least 12, 15, 20, or 25 nucleotides); and (2) nucleic acids containing sequences that hybridize to sequences that are complementary to nucleic acids encoding phytase polypeptides, or fragments thereof (*e.g.*, fragments containing at least 12, 15, 20, or 25 nucleotides) - can be used in methods focused on their hybridization properties. For example, as is described in further detail herein, such nucleic acid molecules can be used in the following methods: PCR methods for synthesizing phytase nucleic acids,



methods for detecting the presence of a phytase nucleic acid in a sample, screening methods for identifying nucleic acids encoding new phytase family members. Hybridization-based uses include Southern-type, Northern-type, RNA protection, and any hybridization procedure where a nucleic acid is used as a hybridization partner.

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Fragments or portions of the polynucleotides of the present invention may be used to synthesize full-length polynucleotides of the present invention. Accordingly, fragments or portions of the enzymes of the present invention may be employed for producing the corresponding full-length enzyme by peptide synthesis; therefore, the fragments may be employed as intermediates for producing the full-length enzymes. Size separation of the cleaved fragments is generally performed using 8 percent polyacrylamide gel as described in the literature (*e.g.* by Goeddel *et al.*, 1980).

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**6.3.15 - Use in Directed Evolution:** This invention provides enzymes, as well as fragments, other derivatives, and analogs thereof, and the corresponding nucleotides for use in directed evolution. The discovery and use of a plurality of templates as disclosed herein may significantly increase the potential yield of directed evolution in comparison to the directed evolution of a single template protein. Hence, the need for discovery is based on the premise that nature provides a wealth of potentially unattainable or unpredictable features in distinct but related members of molecular groupings, and that the exploitation of these features may greatly facilitate directed evolution. Thus, in one aspect, related but distinct molecules may serve as unique starting templates for the directed evolution of a desired characteristic. In another aspect, they may serve as repositories of structure-function information including, but not limited to, a variety of consensus motifs. Both utilities help to obviate the logistically impractical task of at-once exploring an overly wide range of mutational permutations on any given molecule. For example, the full range of mutational permutations on a 100 amino acid protein includes over  $10^{130}$  possibilities (assuming there are 20 amino acid possibilities at each position), a number too large for practical consideration.

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Accordingly, particularly because of logistical and technical constraints, it is a desirable approach - in performing "directed evolution" - to discover and to make use

of a plurality of related starting templates that have pre-evolved differences. These templates can then be subjected to a variety of mutagenic manipulations including, by way of non-limiting exemplification, DNA mutagenesis and combinatorial enzyme development, an approach that is further elaborated in co-pending USPN 5,830,696 (Short *et al.*).

The enzyme activities of the novel molecules generated can then be screened by a variety of methods including, by way of non-limiting exemplification: a) molecular biopanning; b) recombinant clone screening; and c) extract screening.

**6.3.16 - Use in antibody production:** This invention provides enzymes, as well as fragments, other derivatives, and analogs thereof, and cells expressing them that can be used as an immunogen to produce antibodies thereto. These antibodies can be, for example, polyclonal or monoclonal antibodies. The present invention also includes chimeric, single chain, and humanized antibodies, as well as Fab fragments, or the product of an Fab expression library. Various procedures known in the art may be used for the production of such antibodies and fragments.

Antibodies generated against the enzymes corresponding to a sequence of the present invention can be obtained by direct injection of the enzymes into an animal or by administering the enzymes to an animal, preferably a nonhuman. The antibody so obtained will then bind the enzymes itself. In this manner, even a sequence encoding only a fragment of the enzymes can be used to generate antibodies binding the whole native enzymes. Such antibodies can then be used to isolate the enzyme from cells expressing that enzyme.

For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler and Milstein, 1975), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, 1983), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole *et al.*, 1985, pp. 77-96).

Techniques described for the production of single chain antibodies (USPN 4,946,778 Ladner *et al.*) can be adapted to produce single chain antibodies to immunogenic enzyme products of this invention. Also, transgenic mice may be used to express humanized antibodies to immunogenic enzyme products of this invention.

Antibodies generated against the enzyme of the present invention may be used in screening for similar enzymes from other organisms and samples. Such screening techniques are known in the art. Antibodies may also be employed as a probe to screen gene libraries generated from this or other organisms to identify this or cross reactive activities.

Isolation and purification of polypeptides produced in the systems described above can be carried out using conventional methods, appropriate for the particular system. For example, preparative chromatography and immunological separations employing antibodies, such as monoclonal or polyclonal antibodies, can be used.

As is mentioned above, antigens that can be used in producing phytase-specific antibodies include phytase polypeptides, *e.g.*, any of the phytase shown in Figures 1 polypeptide fragments. The polypeptide or peptide used to immunize an animal can be obtained by standard recombinant, chemical synthetic, or purification methods. As is well known in the art, in order to increase immunogenicity, an antigen can be conjugated to a carrier protein. Commonly used carriers include keyhole limpet hemocyanin (KLH), thyroglobulin, bovine serum albumin (BSA), and tetanus toxoid. The coupled peptide is then used to immunize the animal (*e.g.*, a mouse, a rat, or a rabbit). In addition to such carriers, well known adjuvants can be administered with the antigen to facilitate induction of a strong immune response.

Phytase-specific polyclonal and monoclonal antibodies can be purified, for example, by binding to, and elution from, a matrix containing a phytase polypeptide, *e.g.*, the phytase polypeptide (or fragment thereof) to which the antibodies were raised. Additional methods for antibody purification and concentration are well known in the art and can be practiced with the phytase-specific antibodies of the invention (see, *e.g.*, Coligan *et al.*, 1996).

Anti-idiotypic antibodies corresponding to phytase-specific antigens are also included in the invention, and can be produced using standard methods. These antibodies are raised to phytase-specific antibodies, and thus mimic phytase-specific epitopes.

This invention also includes additional uses of fragments of the phytase polypeptides that retain at least one phytase-specific activity or epitope. Phytase activity can be assayed by examining the catalysis of phytate to inositol and free phosphate. Such fragments can easily be identified by comparing the sequences of phytases found in Figure 1.

In a non-limiting exemplification, a phytase polypeptide fragment containing, *e.g.*, at least 8-10 amino acids can be used as an immunogen in the production of phytase-specific antibodies. The fragment can contain, for example, an amino acid sequence that is conserved in phytases, and this amino acid sequence can contain amino acids that are conserved in phytases. In another non-limiting exemplification, the above-described phytase fragments can be used in immunoassays, such as ELISAs, to detect the presence of phytase-specific antibodies in samples.

#### **6.3.17 – Use in transgenics:**

Various methods to make the transgenic animals of the subject invention can be employed. Generally speaking, three such methods may be employed. In one such method, an embryo at the pronuclear stage (a “one cell embryo”) is harvested from a female and the transgene is microinjected into the embryo, in which case the transgene will be chromosomally integrated into both the germ cells and somatic cells of the resulting mature animal. In another such method, embryonic stem cells are isolated and the transgene incorporated therein by electroporation, plasmid transfection or microinjection, followed by reintroduction of the stem cells into the embryo where they colonize and contribute to the germ line. Methods for microinjection of mammalian species is described in U.S. Pat. No. 4,873,191. In yet another such method, embryonic cells are infected with a retrovirus containing the transgene whereby the germ cells of the embryo have the transgene chromosomally integrated therein. When the animals to be made transgenic are avian, because avian fertilized ova generally go through cell

division for the first twenty hours in the oviduct, microinjection into the pronucleus of the fertilized egg is problematic due to the inaccessibility of the pronucleus. Therefore, of the methods to make transgenic animals described generally above, retrovirus infection is preferred for avian species, for example as described in U.S. Pat No.

5 5,162,215. If micro-injection is to be used with avian species, however, a published procedure by Love *et al.*, (Biotechnology, 12, Jan 1994) can be utilized whereby the embryo is obtained from a sacrificed hen approximately two and one-half hours after the laying of the previous laid egg, the transgene is microinjected into the cytoplasm of the germinal disc and the embryo is cultured in a host shell until maturity. When the  
10 animals to be made transgenic are bovine or porcine, microinjection can be hampered by the opacity of the ova thereby making the nuclei difficult to identify by traditional differential interference-contrast microscopy. To overcome this problem, the ova can first be centrifuged to segregate the pronuclei for better visualization.

15 The “non-human animals” of the invention bovine, porcine, ovine and avian animals (*e.g.*, cow, pig, sheep, chicken). The “transgenic non-human animals” of the invention are produced by introducing “transgenes” into the germline of the non-human animal. Embryonal target cells at various developmental stages can be used to introduce transgenes. Different methods are used depending on the stage of development of the  
20 embryonal target cell. The zygote is the best target for micro-injection. The use of zygotes as is target for gene transfer has a major advantage in that in most cases the injected DNA will be incorporated into the host gene before the first cleavage (Brinster *et al.*, Proc. Natl. Acad. Sci. USA 82:4438-4442, 1985). As a consequence, all cells of the transgenic non-human animal will carry the incorporated transgene. This will in  
25 general also be reflected in the efficient transmission of the transgene to offspring of the founder since 50% of the germ cells will harbor the transgene.

The term “transgenic” is used to describe an animal which includes exogenous genetic material within all of its cells. A “transgenic” animal can be produced by cross-  
30 breeding two chimeric animals which include exogenous genetic material within cells used in reproduction. Twenty-five percent of the resulting offspring will be transgenic *i.e.*, animals which include the exogenous genetic material within all of their cells in

both alleles, 50% of the resulting animals will include the exogenous genetic material within one allele and 25% will include no exogenous genetic material.

In the microinjection method useful in the practice of the subject invention, the transgene is digested and purified free from any vector DNA, *e.g.*, by gel electrophoresis. It is preferred that the transgene include an operatively associated promoter which interacts with cellular proteins involved in transcription, ultimately resulting in constitutive expression. Promoters useful in this regard include those from cytomegalovirus (CMV), Moloney leukemia virus (MLV), and herpes virus, as well as those from the genes encoding metallothionin, skeletal actin, P-enolpyruvate carboxylase (PEPCK), phosphoglycerate (PGK), DHFR, and thymidine kinase. Promoters for viral long terminal repeats (LTRs) such as Rous Sarcoma Virus can also be employed. When the animals to be made transgenic are avian, preferred promoters include those for the chicken  $\beta$ -globin gene, chicken lysozyme gene, and avian leukemia virus. Constructs useful in plasmid transfection of embryonic stem cells will employ additional regulatory elements well known in the art such as enhancer elements to stimulate transcription, splice acceptors, termination and polyadenylation signals, and ribosome binding sites to permit translation.

Retroviral infection can also be used to introduce transgene into a non-human animal, as described above. The developing non-human embryo can be cultured *in vitro* to the blastocyst stage. During this time, the blastomeres can be targets for retroviral infection (Jaenich, R., Proc. Natl. Acad. Sci USA 73:1260-1264, 1976). Efficient infection of the blastomeres is obtained by enzymatic treatment to remove the zona pellucida (Hogan, *et al.* (1986) in *Manipulating the Mouse Embryo*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.). The viral vector system used to introduce the transgene is typically a replication-defective retro virus carrying the transgene (Jahner, *et al.*, Proc. Natl. Acad. Sci. USA 82: 6927-6931, 1985; Van der Putten, *et al.*, Proc. Natl. Acad. Sci USA 82: 6148-6152, 1985). Transfection is easily and efficiently obtained by culturing the blastomeres on a monolayer of virus-producing cells (Van der Putten, *supra*; Stewart, *et al.*, EMBO J. 6: 383-388, 1987). Alternatively, infection can be performed at a later stage. Virus or virus-producing cells can be injected into the blastocoele (D. Jahner *et al.*, Nature 298: 623-628, 1982). Most

of the founders will be mosaic for the transgene since incorporation occurs only in a subset of the cells which formed the transgenic nonhuman animal. Further, the founder may contain various retro viral insertions of the transgene at different positions in the genome which generally will segregate in the offspring. In addition, it is also possible to introduce transgenes into the germ line, albeit with low efficiency, by intrauterine retroviral infection of the midgestation embryo (D. Jahner *et al.*, *supra*).

A third type of target cell for transgene introduction is the embryonal stem cell (ES). ES cells are obtained from pre-implantation embryos cultured *in vitro* and fused with embryos (M. J. Evans *et al.*, *Nature* 292:154-156, 1981; M. O. Bradley *et al.*, *Nature* 309:255-258, 1984; Gossler, *et al.*, *Proc. Natl. Acad. Sci USA* 83:9065-9069, 1986; and Robertson *et al.*, *Nature* 322:445-448, 1986). Transgenes can be efficiently introduced into the ES cells by DNA transfection or by retro virus-mediated transduction. Such transformed ES cells can thereafter be combined with blastocysts from a nonhuman animal. The ES cells thereafter colonize the embryo and contribute to the germ line of the resulting chimeric animal. (For review see Jaenisch, R., *Science* 240:1468-1474, 1988).

“Transformed” means a cell into which (or into an ancestor of which) has been introduced, by means of recombinant nucleic acid techniques, a heterologous nucleic acid molecule. “Heterologous” refers to a nucleic acid sequence that either originates from another species or is modified from either its original form or the form primarily expressed in the cell.

“Transgene” means any piece of DNA which is inserted by artifice into a cell, and becomes part of the genome of the organism (*i.e.*, either stably integrated or as a stable extrachromosomal element) which develops from that cell. Such a transgene may include a gene which is partly or entirely heterologous (*i.e.*, foreign) to the transgenic organism, or may represent a gene homologous to an endogenous gene of the organism. Included within this definition is a transgene created by the providing of an RNA sequence which is transcribed into DNA and then incorporated into the genome. The transgenes of the invention include DNA sequences which encode phytases or polypeptides having phytase activity, and include polynucleotides, which may be

expressed in a transgenic non-human animal. The term "transgenic" as used herein additionally includes any organism whose genome has been altered by *in vitro* manipulation of the early embryo or fertilized egg or by any transgenic technology to induce a specific gene knockout. The term "gene knockout" as used herein, refers to the targeted disruption of a gene *in vivo* with complete loss of function that has been achieved by any transgenic technology familiar to those in the art. In one embodiment, transgenic animals having gene knockouts are those in which the target gene has been rendered nonfunctional by an insertion targeted to the gene to be rendered non-functional by homologous recombination. As used herein, the term "transgenic" includes any transgenic technology familiar to those in the art which can produce an organism carrying an introduced transgene or one in which an endogenous gene has been rendered non-functional or "knocked out."

The transgene to be used in the practice of the subject invention is a DNA sequence comprising a sequence coding for a phytase or a polypeptide having phytase activity. In a one embodiment, a polynucleotide having a sequence as set forth in SEQ ID NO:1 or a sequence encoding a polypeptide having a sequence as set forth in SEQ ID NO:2 is the transgene as the term is defined herein. Where appropriate, DNA sequences that encode proteins having phytase activity but differ in nucleic acid sequence due to the degeneracy of the genetic code may also be used herein, as may truncated forms, allelic variants and interspecies homologues.

After an embryo has been microinjected, colonized with transfected embryonic stem cells or infected with a retrovirus containing the transgene (except for practice of the subject invention in avian species which is addressed elsewhere herein) the embryo is implanted into the oviduct of a pseudopregnant female. The consequent progeny are tested for incorporation of the transgene by Southern blot analysis of blood or tissue samples using transgene specific probes. PCR is particularly useful in this regard. Positive progeny (G0) are crossbred to produce offspring (G1) which are analyzed for transgene expression by Northern blot analysis of tissue samples.

Thus, the present invention includes methods for increasing the phosphorous uptake in the transgenic animal and/or decreasing the amount of pollutant in the manure



of the transgenic organism by about 15%, typically about 20%, and more typically about 20% to about 50%.

The animals contemplated for use in the practice of the subject invention are those animals generally regarded as domesticated animals including pets (*e.g.*, canines, felines, avian species *etc.*) and those useful for the processing of food stuffs, *i.e.*, avian such as meat bred and egg laying chicken and turkey, ovine such as lamb, bovine such as beef cattle and milk cows, piscine and porcine. For purposes of the subject invention, these animals are referred to as “transgenic” when such animal has had a heterologous DNA sequence, or one or more additional DNA sequences normally endogenous to the animal (collectively referred to herein as “transgenes”) chromosomally integrated into the germ cells of the animal. The transgenic animal (including its progeny) will also have the transgene fortuitously integrated into the chromosomes of somatic cells.

#### 6.3.18 – Uses in gene delivery:

In some instances it may be advantageous to deliver and express a phytase sequence of the invention locally (*e.g.*, within a particular tissue or cell type). For example, local expression of a phytase or digestive enzyme in the gut of an animal will assist in the digestion and uptake of, for example, phytate and phosphorous, respectively. The nucleic sequence may be directly delivered to the salivary glands, tissue and cells and/or to the epithelial cells lining the gut, for example. Such delivery methods are known in the art and include electroporation, viral vectors and direct DNA uptake. Any polypeptide having phytase activity can be utilized in the methods of the invention (*e.g.*, those specifically described under this subsection 6.3.18, as well as those described in other sections of the invention).

For example, a nucleic acid constructs of the present invention will comprise nucleic acid molecules in a form suitable for uptake into target cells within a host tissue. The nucleic acids may be in the form of bare DNA or RNA molecules, where the molecules may comprise one or more structural genes, one or more regulatory genes, antisense strands, strands capable of triplex formation, or the like. Commonly, the nucleic acid construct will include at least one structural gene under the transcriptional and translational control of a suitable regulatory region. More usually, nucleic acid

constructs of the present invention will comprise nucleic acids incorporated in a delivery vehicle to improve transfection efficiency, wherein the delivery vehicle will be dispersed within larger particles comprising a dried hydrophilic excipient material.

5 One such delivery vehicles comprises viral vectors, such as retroviruses, adenoviruses, and adeno-associated viruses, which have been inactivated to prevent self-replication but which maintain the native viral ability to bind a target host cell, deliver genetic material into the cytoplasm of the target host cell, and promote expression of structural or other genes which have been incorporated in the particle.

10 Suitable retrovirus vectors for mediated gene transfer are described in Kahn *et al.* (1992) CIRC. RES. 71:1508-1517, the disclosure of which is incorporated herein by reference. A suitable adenovirus gene delivery is described in Rosenfeld *et al.* (1991) SCIENCE 252:431-434, the disclosure of which is incorporated herein by reference. Both retroviral and adenovirus delivery systems are described in Friedman (1989)

15 SCIENCE 244:1275-1281, the disclosure of which is also incorporated herein by reference.

A second type of nucleic acid delivery vehicle comprises liposomal transfection vesicles, including both anionic and cationic liposomal constructs. The use of anionic

20 liposomes requires that the nucleic acids be entrapped within the liposome. Cationic liposomes do not require nucleic acid entrapment and instead may be formed by simple mixing of the nucleic acids and liposomes. The cationic liposomes avidly bind to the negatively charged nucleic acid molecules, including both DNA and RNA, to yield complexes which give reasonable transfection efficiency in many cell types. See,

25 Farhood *et al.* (1992) BIOCHEM. BIOPHYS. ACTA. 1111:239-246, the disclosure of which is incorporated herein by reference. A particularly preferred material for forming liposomal vesicles is lipofectin which is composed of an equimolar mixture of dioleylphosphatidyl ethanolamine (DOPE) and dioleoyloxypropyl-triethylammonium (DOTMA), as described in Felgner and Ringold (1989) NATURE 337:387-388, the

30 disclosure of which is incorporated herein by reference.

It is also possible to combine these two types of delivery systems. For example, Kahn *et al.* (1992), *supra.*, teaches that a retrovirus vector may be combined in a

cationic DEAE-dextran vesicle to further enhance transformation efficiency. It is also possible to incorporate nuclear proteins into viral and/or liposomal delivery vesicles to even further improve transfection efficiencies. See, Kaneda *et al.* (1989) SCIENCE 243:375-378, the disclosure of which is incorporated herein by reference.

5

#### **6.3.19 – Use in dietary aids:**

In another embodiment, a digestive aid containing an enzyme either as the sole active ingredient or in combination with one or more other agents and/or enzymes is provided (as described in co-pending application U.S. Serial No. \_\_\_\_\_, entitled

10 “Dietary Aids and Methods of Use Thereof,” filed May 25, 2000, the disclosure of which is incorporated herein by reference in its entirety). The use of enzymes and other agents in digestive aids of livestock or domesticated animals not only improves the animal’s health and life expectancy but also assists in increasing the health of livestock and in the production of foodstuffs from livestock.

15

Currently, some types of feed for livestock (*e.g.*, certain poultry feed) are highly supplemented with numerous minerals (*e.g.*, inorganic phosphorous), enzymes, growth factors, drugs, and other agents for delivery to the livestock. These supplements replace many of the calories and natural nutrients present in grain, for example.

20

By reducing or eliminating the inorganic phosphorous supplement and other supplements (*e.g.*, trace mineral salts, growth factors, enzymes, antibiotics) from the feed itself, the feed would be able to carry more nutrient and energy. Accordingly, the remaining diet would contain more usable energy. For example, grain-oilseed meal

25 diets generally contain about 3,200 kcal metabolizable energy per kilogram of diet, and mineral salts supply no metabolizable energy. Removal of the unneeded minerals and substitution with grain would therefore increase the usable energy in the diet. Thus, the invention can be differentiated over commonly used phytase containing feed. For example, in one embodiment, a biocompatible material is used that is resistant to

30 digestion by the gastrointestinal tract of an organism.

In many organisms, including, for example, poultry or birds such as, for example, chickens, turkeys, geese, ducks, parrots, peacocks, ostriches, pheasants, quail,

pigeons, emu, kiwi, loons, cockatiel, cockatoo, canaries, penguins, flamingoes, and dove, the digestive tract includes a gizzard which stores and uses hard biocompatible objects (*e.g.*, rocks and shells from shell fish) to help in the digestion of seeds or other feed consumed by a bird. A typical digestive tract of this general family of organisms, includes the esophagus which contains a pouch, called a crop, where food is stored for a brief period of time. From the crop, food moves down into the true stomach, or *proventriculus*, where hydrochloric acid and pepsin starts the process of digestion. Next, food moves into the gizzard, which is oval shaped and thick walled with powerful muscles. The chief function of the gizzard is to grind or crush food particles - a process which is aided by the bird swallowing small amounts of fine gravel or grit. From the gizzard, food moves into the duodenum. The small intestine of birds is similar to mammals. There are two blind pouches or *ceca*, about 4-6 inches in length at the junction of the small and large intestine. The large intestine is short, consisting mostly of the rectum about 3-4 inches in length. The rectum empties into the *cloaca* and feces are excreted through the vent.

Hard, biocompatible objects consumed (or otherwise introduced) and presented in the gizzard provide a useful vector for delivery of various enzymatic, chemical, therapeutic and antibiotic agents. These hard substances have a life span of a few hours to a few days and are passed after a period of time. Accordingly, the invention provides coated, impregnated (*e.g.*, impregnated matrix and membranes) modified dietary aids for delivery of useful digestive or therapeutic agents to an organism. Such dietary aids include objects which are typically ingested by an organism to assist in digestion within the gizzard (*e.g.*, rocks or grit). The invention provides biocompatible objects that have coated thereon or impregnated therein agents useful as a digestive aid for an organism or for the delivery of a therapeutic or medicinal agent or chemical.

In a first embodiment, the invention provides a dietary aid, having a biocompatible composition designed for release of an agent that assists in digestion, wherein the biocompatible composition is designed for oral consumption and release in the digestive tract (*e.g.*, the gizzard) of an organism. "Biocompatible" means that the substance, upon contact with a host organism (*e.g.*, a bird), does not elicit a detrimental response sufficient to result in the rejection of the substance or to render the substance

inoperable. Such inoperability may occur, for example, by formation of a fibrotic structure around the substance limiting diffusion of impregnated agents to the host organism therein or a substance which results in an increase in mortality or morbidity in the organism due to toxicity or infection. A biocompatible substance may be non-  
5 biodegradable or biodegradable. In one embodiment, the biocompatible composition is resistant to degradation or digestion by the gastrointestinal tract. In another embodiment, the biocompatible composition has the consistency of a rock or stone.

A non-biodegradable material useful in the invention is one that allows  
10 attachment or impregnation of a dietary agent. Such non-biodegradable materials include, for example, thermoplastics, such as acrylic, modacrylic, polyamide, polycarbonate, polyester, polyethylene, polypropylene, polystyrene, polysulfone, polyethersulfone, and polyvinylidene fluoride. Elastomers are also useful materials and include, for example, polyamide, polyester, polyethylene, polypropylene, polystyrene,  
15 polyurethane, polyvinyl alcohol and silicone (*e.g.*, silicone based or containing silica). The invention provides that the biocompatible composition can contain a plurality of such materials, which can be, *e.g.*, admixed or layered to form blends, copolymers or combinations thereof.

As used herein, a "biodegradable" material means that the composition will  
20 erode or degrade *in vivo* to form smaller chemical species. Degradation may occur, for example, by enzymatic, chemical or physical processes. Suitable biodegradable materials contemplated for use in the invention include poly(lactide)s, poly(glycolide)s, poly(lactic acid)s, poly(glycolic acid)s, polyanhydrides, polyorthoesters,  
25 polyetheresters, polycaprolactone, polyesteramides, polycarbonate, polycyanoacrylate, polyurethanes, polyacrylate. Such materials can be admixed or layered to form blends, copolymers or combinations thereof.

It is contemplated that a number different biocompatible substances may be  
30 ingested or otherwise provided to the same organism simultaneously, or in various combinations (*e.g.*, one material before the other). In addition, the biocompatible substance may be designed for slow passage through the digestive tract. For example, large or fatty substances tend to move more slowly through the digestive tract,

accordingly, a biocompatible material having a large size to prevent rapid passing in the digestive tract can be used. Such large substances can be a combination of non-biodegradable and biodegradable substances. For example, a small non-biodegradable substance can be encompassed by a biodegradable substance such that over a period of time the biodegradable portion will be degraded allowing the non-biodegradable portion to pass through the digestive trace. In addition, it is recognized that any number of flavorings can be provided to the biocompatible substance to assist in consumption.

Any number of agents alone or in combination with other agents can be coated on the biocompatible substance including polypeptides (*e.g.*, enzymes, antibodies, cytokines or therapeutic small molecules), and antibiotics, for example. Examples of particular useful agents are listed in Table 1 and 2, below. It is also contemplated that cells can be encapsulated into the biocompatible material of the invention and used to deliver the enzymes or therapeutics. For example, porous substances can be designed that have pores large enough for cells to grow in and through and that these porous materials can then be taken into the digestive tract. For example, the biocompatible substance can be comprised of a plurality of microfloral environments (*e.g.*, different porosity, pH etc.) that provide support for a plurality of cell types. The cells can be genetically engineered to deliver a particular drug, enzyme or chemical to the organism. The cells can be eukaryotic or prokaryotic.

TABLE 1

| Treatment Class | Chemical   | Description   |
|-----------------|--|---|
| Antibiotics     | Amoxycillin and Its Combination<br>Mastox Injection<br>(Amoxycillin and Cloxacillin) | Treatment Against Bacterial Diseases Caused By Gram + and Gram – Bacteria                                 |
|                 | Ampicillin and Its Combination<br>BioloX Injection<br>(Ampicillin and Cloxacillin)   | Treatment Against Bacterial Diseases Caused By Gram + And Gram – Bacteria.                                |
|                 | Nitrofurazone + Urea<br>Nefrea Bolus   | Treatment Of Genital Infections   |
|                 | Trimethoprim +<br>Sulphamethoxazole<br>Trizol Bolus                                  | Treatment Of Respiratory Tract Infections, Gastro Intestinal Tract Infections, Urino- Genital Infections. |
|                 | Metronidazole and Furazolidone<br>Metofur Bolus                                      | Treatment Of Bacterial And Protozoal Diseases.  |

|                                |  |   |
|--------------------------------|--|---|
|                                | Phthalylsulphathiazole, Pectin and Kaolin<br>Pectolin<br>Bolus<br>Suspension   | Treatment Of Bacterial And Non-Specific Diarrhoea, Bacillary Dysentery And Calf Scours.   |
| <b>Antihelmintics</b>          | Ectoparasiticide<br>Germex Ointment<br>(Gamma Benzene Hexachloride, Proflavin Hemisulphate and Cetrimide)  | Ectoparasiticide and Antiseptic   |
|                                | Endoparasiticides > Albendazole and Its Combination<br>Alben ( Albendazole)<br>Suspension (Albendazole 2.5%)<br>Plus Suspension (Albendazole 5%)<br>Forte Bolus (Albendazole 1.5 Gm.)<br>Tablet (Albendazole 600 Mg.)<br>Powder(Albendazole 5%, 15%) | Prevention And Treatment Of Roundworm, Tapeworm and Fluke Infestations  |
|                                | Alpraz ( Albendazole and Praziquantel)Tablet   | Prevention And Treatment Of Roundworm and Tapeworm Infestation In Canines and Felines.  |
|                                | Oxyclozanide and Its Combination<br>Clozan ( Oxyclozanide) Bolus, Suspension   | Prevention and Treatment Of Fluke Infestations  |
|                                | Tetzan ( Oxyclozanide and Tetramisole Hcl ) Bolus, Suspension  | Prevention and Treatment Of Roundworm and Fluke Infestations  |
|                                | Fluzan ( Oxyclozanide and Levamisole Hcl) Bolus, Suspension  | Prevention and Treatment Of Roundworm Infestations and Increasing Immunity  |
|                                | Levamisole<br>Nemasol Injection<br>Wormnil Powder  | Prevention and Treatment Of Roundworm Infestations and Increasing Immunity.   |
|                                | Fenbendazole<br>Fenzole<br>Tablet ( Fenbendazole 150 Mg.)<br>Bolus ( Fenbendazole 1.5 Gm.)<br>Powder ( Fenbendazole 2.5% W/W)  | Prevention And Treatment of Roundworm and Tapeworm Infestations   |
| <b>Tonics</b>                  | Vitamin B Complex, Amino Acids and Liver Extract<br>Heptogen Injection   | Treatment Of Anorexia, Hepatitis, Debility, Neuralgic Convulsions Emaciation and Stunted Growth.  |
|                                | Calcium Levulinate With Vit.B <sub>12</sub> and Vit D <sub>3</sub><br>Hylactin Injection   | Prevention and treatment of hypocalcaemia, supportive therapy in sick conditions (especially hypothermia) and treatment of early stages of rickets. |
| <b>Animal Feed Supplements</b> | Essential Minerals, Selenium and Vitamin E<br>Gynolactin Bolus   | Treatment Of Anoestrus Causing Infertility and Repeat Breeding In Dairy Animals and Horses.   |
|                                | Essential Minerals, Vitamin E, and Iodine<br>Hylactin Powder   | Infertility, Improper Lactation, Decreased Immunity, Stunted Growth and Debility.   |
|                                | Essential Electrolytes With Vitamin C<br>Electra – C Powder  | Diarrhoea, Dehydration, Prior to and after Transportation, In Extreme temperatures (High Or Low) and other Conditions of stress.                    |

|  |   |
|--|---|
| Pyrenox Plus ( Diclofenac Sodium + Paracetamol ) Bolus, Injection. | Treatment Of Mastitis, Pyrexia Post Surgical Pain and Inflammation, Prolapse Of Uterus, Lameness and Arthritis. |
|--|---|

**Table 2. Therapeutic Formulations**

| Product   | Description  |
|---|--|
| <b>Acutrim®</b><br>(phenylpropanolamine)                                    | Once-daily appetite suppressant tablets.   |
| <b>The Baxter® Infusor</b>  | For controlled intravenous delivery of anticoagulants, antibiotics, chemotherapeutic agents, and other widely used drugs.  |
| <b>Catapres-TTS®</b> (clonidine transdermal therapeutic system)             | Once-weekly transdermal system for the treatment of hypertension.  |
| <b>Covera HS™</b> (verapamil hydrochloride)                                 | Once-daily Controlled-Onset Extended-Release (COER-24) tablets for the treatment of hypertension and angina pectoris.  |
| <b>DynaCirc CR®</b> (isradipine)  | Once-daily extended release tablets for the treatment of hypertension.   |
| <b>Efidac 24®</b> (chlorpheniramine maleate)                                | Once-daily extended release tablets for the relief of allergy symptoms.  |
| <b>Estraderm®</b><br>(estradiol transdermal system)                         | Twice-weekly transdermal system for treating certain postmenopausal symptoms and preventing osteoporosis   |
| <b>Glucotrol XL®</b> (glipizide)  | Once-daily extended release tablets used as an adjunct to diet for the control of hyperglycemia in patients with non-insulin-dependent diabetes mellitus.  |
| <b>IVOMEC SR® Bolus</b><br>(ivermectin)                                     | Ruminal delivery system for season-long control of major internal and external parasites in cattle.  |
| <b>Minipress XL®</b> (prazosin)   | Once-daily extended release tablets for the treatment of hypertension.   |
| <b>NicoDerm® CQ™</b> (nicotine transdermal system)                          | Transdermal system used as a once-daily aid to smoking cessation for relief of nicotine withdrawal symptoms.   |
| <b>Procardia XL®</b> (nifedipine)   | Once-daily extended release tablets for the treatment of angina and hypertension.  |
| <b>Sudafed® 24 Hour</b><br>(pseudoephedrine)                                | Once-daily nasal decongestant for relief of colds, sinusitis, hay fever and other respiratory allergies.   |
| <b>Transderm-Nitro®</b> (nitroglycerin transdermal system)                  | Once-daily transdermal system for the prevention of angina pectoris due to coronary artery disease.  |
| <b>Transderm Scop®</b> (scopolamin transdermal system)                      | Transdermal system for the prevention of nausea and vomiting associated with motion sickness.  |
| <b>Volmax</b> (albuterol)   | Extended release tablets for relief of bronchospasm in patients with reversible obstructive airway disease.  |
| <b>Actisite®</b>  | (tetracycline hydrochloride) Periodontal fiber used as an adjunct to scaling and root planing for reduction of pocket depth and bleeding on probing in patients with adult periodontitis.  |
| <b>ALZET®</b>   | Osmotic pumps for laboratory research.   |
| <b>Amphotec®</b> (amphotericin B cholesteryl sulfate complex for injection) | AMPHOTEC® is a fungicidal treatment for invasive aspergillosis in patients where renal impairment or unacceptable toxicity precludes use of amphotericin B in effective doses and in patients with invasive aspergillosis where prior amphotericin B therapy has failed. |
| <b>BiCitra®</b> (sodium citrate and citric acid)                            | Alkalinizing agent used in those conditions where long-term maintenance of alkaline urine is desirable.  |
| <b>Ditropan®</b> (oxybutynin chloride)                                      | For the relief of symptoms of bladder instability associated with uninhibited neurogenic or reflex neurogenic bladder ( <i>i.e.</i> , urgency, frequency, urinary leakage, urge incontinence, dysuria).  |
| <b>Ditropan® XL</b> (oxybutynin chloride)                                   | is a once-daily controlled-release tablet indicated for the treatment of overactive bladder with symptoms of urge urinary incontinence, urgency and frequency.   |
| <b>DOXIL®</b> (doxorubicin HCl liposome injection)                          |  |



|   |   |
|---|---|
| <b>Duragesic®</b> (fentanyl transdermal system) CII   | 72-hour transdermal system for management of chronic pain in patients who require continuous opioid analgesia for pain that cannot be managed by lesser means such as acetaminophen-opioid combinations, non-steroidal analgesics, or PRN dosing with short-acting opioids.   |
| <b>Elmiron®</b> (pentosan polysulfate sodium)   | Indicated for the relief of bladder pain or discomfort associated with interstitial cystitis.   |
| <b>ENACT AirWatch™</b>  | An asthma monitoring and management system.   |
| <b>Ethyol®</b> (amifostine)   | Indicated to reduce the cumulative renal toxicity associated with repeated administration of cisplatin in patients with advanced ovarian cancer or non-small cell lung cancer.<br>Indicated to reduce the incidence of moderate to severe xerostomia in patients undergoing post-operative radiation treatment for head and neck cancer, where the radiation port includes a substantial portion of the parotid glands. |
| <b>Mycelex® Troche</b> (clotrimazole)   | For the local treatment of oropharyngeal candidiasis. Also indicated prophylactically to reduce the incidence of oropharyngeal candidiasis in patients immunocompromised by conditions that include chemotherapy, radiotherapy, or steroid therapy utilized in the treatment of leukemia, solid tumors, or renal transplantation.   |
| <b>Neutra-Phos®</b> (potassium and sodium phosphate)  | a dietary/nutritional supplement  |
| <b>PolyCitra® -K Oral Solution and PolyCitra® -K Crystals</b> (potassium citrate and citric acid) | Alkalinizing agent useful in those conditions where long-term maintenance of an alkaline urine is desirable, such as in patents with uric acid and cystine calculi of the urinary tract, especially when the administration of sodium salts is undesirable or contraindicated   |
| <b>PolyCitra® -K Syrup and LC</b> (tricitrates)   | Alkalinizing agent useful in those conditions where long-term maintenance of an alkaline urine is desirable, such as in patients with uric acid and cystine calculi of the urinary tract.   |
| <b>Progestasert®</b> (progesterone)   | Intrauterine Progesterone Contraceptive System  |
| <b>Testoderm® Testoderm® with Adhesive and Testoderm® TTS CIII</b>                                | Testosterone Transdermal System<br>The Testoderm® products are indicated for replacement therapy in males for conditions associated with a deficiency or absence of endogenous testosterone: (1) Primary hypogonadism (congenital or acquired) or (2) Hypogonadotropic hypogonadism (congenital or acquired).   |
| <b>Viadur™</b> (leuprolide acetate implant)   | Once-yearly implant for the palliative treatment of prostate cancer   |

Certain agents can be designed to become active or in activated under certain conditions (*e.g.*, at certain pH's, in the presence of an activating agent etc.). In addition, it may be advantageous to use pro-enzymes in the compositions of the invention. For example, a pro-enzymes can be activated by a protease (*e.g.*, a salivary protease that is present in the digestive tract or is artificially introduced into the digestive tract of an organism). It is contemplated that the agents delivered by the biocompatible compositions of the invention can be activated or inactivated by the addition of an activating agent which may be ingested by, or otherwise delivered to, the organism. Another mechanism for control of the agent in the digestive tract is an environment sensitive agent that is activated in the proper digestive compartment. For example, an agent may be inactive at low pH but active at neutral pH. Accordingly, the

agent would be inactive in the gut but active in the intestinal tract. Alternatively, the agent can become active in response to the presence of a microorganism specific factor (*e.g.*, microorganisms present in the intestine).

5 In summary, the potential benefits of the present invention include, for example, (1) reduction in or possible elimination of the need for mineral supplements (*e.g.*, inorganic phosphorous supplements), enzymes, or therapeutic drugs for animal (including fish) from the daily feed or grain thereby increasing the amount of calories and nutrients present in the feed, and (2) increased health and growth of domestic and  
10 non-domestic animals including, for example, poultry, porcine, bovine, equine, canine, and feline animals.

A large number of enzymes can be used in the methods and compositions of the present invention. These enzymes include enzymes necessary for proper digestion of  
15 consumed foods, or for proper metabolism, activation or derivation of chemicals, prodrugs or other agents or compounds delivered to the animal via the digestive tract. Examples of enzymes that can be delivered or incorporated into the compositions of the invention, include, for example, feed enhancing enzymes selected from the group consisting of  $\alpha$ -galactosidases,  $\beta$ -galactosidases, in particular lactases, phytases,  $\beta$ -  
20 glucanases, in particular endo- $\beta$ -1,4-glucanases and endo- $\beta$ -1,3(4)-glucanases, cellulases, xylosidases, galactanases, in particular arabinogalactan endo-1,4- $\beta$ -galactosidases and arabinogalactan endo-1,3- $\beta$ -galactosidases, endoglucanases, in particular endo-1,2- $\beta$ -glucanase, endo-1,3- $\alpha$ -glucanase, and endo-1,3- $\beta$ -glucanase, pectin degrading enzymes, in particular pectinases, pectinesterases, pectin lyases,  
25 polygalacturonases, arabinanases, rhamnogalacturonases, rhamnogalacturonan acetyl esterases, rhamnogalacturonan- $\alpha$ -rhamnosidase, pectate lyases, and  $\alpha$ -galacturonisidases, mannanases,  $\beta$ -mannosidases, mannan acetyl esterases, xylan acetyl esterases, proteases, xylanases, arabinoxylanases and lipolytic enzymes such as lipases, phospholipases and cutinases. Phytases as set forth in SEQ ID NO:1 and 2 and in Table  
30 3 below are preferred. The sequences described in Table 3 are SEQ ID NO:1 and 2 having the amino acid substitutions and nucleotide substitutions as described therein.

TABLE 3

| Designation              | Source               | AA seq                                  | Nuc. Sequence   |
|--------------------------|----------------------|---|---|
| E. coli B<br>(reference) | E. coli B            | S10; P26; D176;<br>M298;A299;G312; I428 |   |
| 868PH1                   | Bison E. coli        | I428T                                   |   |
| 872PH1                   | Kangaroo rat E. coli | D176G; G312S<br>M298K; A299T            | GAC(176)GGC; GGT(312)AGT;<br>ATG(298)AAG; GCA(299)ACA |
| 875PH2                   | E. coli W            | A160S;D176G;<br>M298K; A299T            | GCG(160)TCG; GAC(176)GGC;<br>ATG(298)AAG; GCA(299)ACA |
| 873PH1                   | Calf E. coli         | I428R                                   |   |
| E. coli B                | E. coli B            | K298M; T299A                            | AAG(298)ATG; ACA(299)GCA                              |
| K12 appA                 | E. coli K12          | M298K;A299T                             | ATG(298)AAG; GCA(299)ACA                              |

The enzymes used in the invention can be modified to enhance their activity, delivery, activation and degradation. Such modifications can be performed *in vivo* or *in vitro* and use methods and processes generally known in the art as described more fully below. Such methodology generally uses polynucleotide or polypeptide sequences that are either synthesized by automated machines or are cloned, expressed, or manipulated by recombinant DNA techniques.

In a preferred embodiment, the enzyme used in the compositions (*e.g.*, a dietary aid) of the present invention is a phytase enzyme which is stable to heat and is heat resistant and catalyzes the enzymatic hydrolysis of phytate, *i.e.*, the enzyme is able to renature and regain activity after a brief (*i.e.*, 5 to 30 seconds), or longer period, for example, minutes or hours, exposure to temperatures of above 50 °C.

A “feed” and a “food,” respectively, means any natural or artificial diet, meal or the like or components of such meals intended or suitable for being eaten, taken in, digested, by an animal and a human being, respectively. “Dietary Aid,” as used herein, denotes, for example, a composition containing agents that provide a therapeutic or digestive agent to an animal or organism. A “dietary aid,” typically is not a source of caloric intake for an organism, in other words, a dietary aid typically is not a source of energy for the organism, but rather is a composition which is taken in addition to typical “feed” or “food”.

An agent or enzyme (*e.g.*, a phytase) may exert its effect *in vitro* or *in vivo*, *i.e.* before intake or in the stomach or gizzard of the organism, respectively. Also a combined action is possible.

Although any enzyme may be incorporated into a dietary aid, reference is made herein to phytase as an exemplification of the methods and compositions of the invention. A dietary aid of the invention includes an enzyme (*e.g.*, a phytase).

5 Generally, a dietary aid containing a phytase composition is liquid or dry.

Liquid compositions need not contain anything more than the enzyme (*e.g.* a phytase), preferably in a highly purified form. Usually, however, a stabilizer such as glycerol, sorbitol or mono propylen glycol is also added. The liquid composition may  
10 also comprise other additives, such as salts, sugars, preservatives, pH-adjusting agents, proteins, phytate (a phytase substrate). Typical liquid compositions are aqueous or oil-based slurries. The liquid compositions can be added to a biocompatible composition for slow release. Preferably the enzyme is added to a dietary aid composition that is a biocompatible material (*e.g.*, biodegradable or non-biodegradable) and includes the  
15 addition of recombinant cells into, for example, porous microbeads.

Dry compositions may be spray dried compositions, in which case the composition need not contain anything more than the enzyme in a dry form. Usually, however, dry compositions are so-called granulates which may readily be mixed with a  
20 food or feed components, or more preferably, form a component of a pre-mix. The particle size of the enzyme granulates preferably is compatible with that of the other components of the mixture. This provides a safe and convenient means of incorporating enzymes into animal feed. Preferably the granulates are biocompatible and more preferably they biocompatible granulates are non-biodegradable.

25

Agglomeration granulates coated by an enzyme can be prepared using agglomeration technique in a high shear mixer. Absorption granulates are prepared by having cores of a carrier material to absorb/be coated by the enzyme. Preferably the carrier material is a biocompatible non-biodegradable material that simulates the role of  
30 stones or grit in the gizzard of an animal. Typical filler materials used in agglomeration techniques include salts, such as disodium sulphate. Other fillers are kaolin, talc, magnesium aluminium silicate and cellulose fibres. Optionally, binders such as dextrans are also included in agglomeration granulates. The carrier materials can be any

biocompatible material including biodegradable and non-biodegradable materials (*e.g.*, rocks, stones, ceramics, various polymers). Optionally, the granulates are coated with a coating mixture. Such mixture comprises coating agents, preferably hydrophobic coating agents, such as hydrogenated palm oil and beef tallow, and if desired other additives, such as calcium carbonate or kaolin.

Additionally, the dietary aid compositions (*e.g.*, phytase dietary aid compositions) may contain other substituents such as colouring agents, aroma compounds, stabilizers, vitamins, minerals, other feed or food enhancing enzymes etc.

A typical additive usually comprises one or more compounds such as vitamins, minerals or feed enhancing enzymes and suitable carriers and/or excipients.

In a one embodiment, the dietary aid compositions of the invention additionally comprises an effective amount of one or more feed enhancing enzymes, in particular feed enhancing enzymes selected from the group consisting of  $\alpha$ -galactosidases,  $\beta$ -galactosidases, in particular lactases, other phytases,  $\beta$ -glucanases, in particular endo- $\beta$ -1,4-glucanases and endo- $\beta$ -1,3(4)-glucanases, cellulases, xylosidases, galactanases, in particular arabinogalactan endo-1,4- $\beta$ -galactosidases and arabinogalactan endo-1,3- $\beta$ -galactosidases, endoglucanases, in particular endo-1,2- $\beta$ -glucanase, endo-1,3- $\alpha$ -glucanase, and endo-1,3- $\beta$ -glucanase, pectin degrading enzymes, in particular pectinases, pectinesterases, pectin lyases, polygalacturonases, arabinanases, rhamnogalacturonases, rhamnogalacturonan acetyl esterases, rhamnogalacturonan- $\alpha$ -rhamnosidase, pectate lyases, and  $\alpha$ -galacturonisidases, mannanases,  $\beta$ -mannosidases, mannan acetyl esterases, xylan acetyl esterases, proteases, xylanases, arabinoxylanases and lipolytic enzymes such as lipases, phospholipases and cutinases.

The animal dietary aid of the invention is supplemented to the mono-gastric animal before or simultaneously with the diet. In one embodiment, the dietary aid of the invention is supplemented to the mono-gastric animal simultaneously with the diet. In another embodiment, the dietary aid is added to the diet in the form of a granulate or a stabilized liquid.

An effective amount of an enzyme in a dietary aid of the invention is from about 10-20,000; preferably from about 10 to 15,000, more preferably from about 10 to 10,000, in particular from about 100 to 5,000, especially from about 100 to about 2,000 FYT/kg dietary aid.

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Examples of other specific uses of the phytase of the invention is in soy processing and in the manufacture of inositol or derivatives thereof.

10 The invention also relates to a method for reducing phytate levels in animal manure, wherein the animal is fed a dietary aid containing an effective amount of the phytase of the invention. As stated in the beginning of the present application one important effect thereof is to reduce the phosphate pollution of the environment.

15 In another embodiment, the dietary aid is a magnetic carrier. For example, a magnetic carrier containing an enzyme (*e.g.*, a phytase) distributed in, on or through a magnetic carrier (*e.g.*, a porous magnetic bead), can be distributed over an area high in phytate and collected by magnets after a period of time. Such distribution and recollection of beads reduces additional pollution and allows for reuse of the beads. In addition, use of such magnetic beads *in vivo* allows for the localization of the dietary aid to a point in the digestive tract where, for example, phytase activity can be carried out. For example, a dietary aid of the invention containing digestive enzymes (*e.g.*, a phytase) can be localized to the gizzard of the animal by juxtapositioning a magnet next to the gizzard of the animal after the animal consumes a dietary aid of magnetic carriers. The magnet can be removed after a period of time allowing the dietary aid to pass through the digestive tract. In addition, the magnetic carriers are suitable for removal from the organism after sacrificing or to aid in collection.

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When the dietary aid is a porous particle, such particles are typically impregnated by a substance with which it is desired to release slowly to form a slow release particle. Such slow release particles may be prepared not only by impregnating the porous particles with the substance it is desired to release, but also by first dissolving the desired substance in the first dispersion phase. In this case, slow release particles prepared by the method in which the substance to be released is first dissolved

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in the first dispersion phase are also within the scope and spirit of the invention. The porous hollow particles may, for example, be impregnated by a slow release substance such as a medicine, agricultural chemical or enzyme. In particular, when porous hollow particles impregnated by an enzyme are made of a biodegradable polymers, the particles themselves may be used as an agricultural chemical or fertilizer, and they have no adverse effect on the environment. In one embodiment the porous particles are magnetic in nature.

The porous hollow particles may be used as a bioreactor support, in particular an enzyme support. Therefore, it is advantageous to prepare the dietary aid utilizing a method of a slow release, for instance by encapsulating the enzyme of agent in a microvesicle, such as a liposome, from which the dose is released over the course of several days, preferably between about 3 to 20 days. Alternatively, the agent (*e.g.*, an enzyme) can be formulated for slow release, such as incorporation into a slow release polymer from which the dosage of agent (*e.g.*, enzyme) is slowly released over the course of several days, for example from 2 to 30 days and can range up to the life of the animal.

As is known in the art, liposomes are generally derived from phospholipids or other lipid substances. Liposomes are formed by mono- or multilamellar hydrated liquid crystals that are dispersed in an aqueous medium. Any non-toxic, physiologically acceptable and metabolizable lipid capable of forming liposomes can be used. The present compositions in liposome form can contain stabilizers, preservatives, excipients, and the like in addition to the agent. The preferred lipids are the phospholipids and the phosphatidyl cholines (lecithins), both natural and synthetic. Methods to form liposomes are known in the art. See, for example, Prescott, Ed., Methods in Cell Biology, Volume XIV, Academic Press, New York, N.Y. (1976), p. 33 et seq.

Also within the scope of the invention is the use of a phytase of the invention during the preparation of food or feed preparations or additives, *i.e.*, the phytase exerts its phytase activity during the manufacture only and is not active in the final food or feed product. This aspect is relevant for instance in dough making and baking.

Accordingly, phytase or recombinant yeast expressing phytase can be impregnated in, on or through a magnetic carriers, distributed in the dough or food medium, and retrieved by magnets.

5           The dietary aid of the invention may be administered alone to animals in an biocompatible (*e.g.*, a biodegradable or non-biodegradable) carrier or in combination with other digestion additive agents. The dietary aid of the invention thereof can be readily administered as a top dressing or by mixing them directly into animal feed or provided separate from the feed, by separate oral dosage, by injection or by transdermal  
10 means or in combination with other growth related edible compounds, the proportions of each of the compounds in the combination being dependent upon the particular organism or problem being addressed and the degree of response desired. It should be understood that the specific dietary dosage administered in any given case will be adjusted in accordance with the specific compounds being administered, the problem to  
15 be treated, the condition of the subject and the other relevant facts that may modify the activity of the effective ingredient or the response of the subject, as is well known by those skilled in the art. In general, either a single daily dose or divided daily dosages may be employed, as is well known in the art.

20           If administered separately from the animal feed, forms of the dietary aid can be prepared by combining them with non-toxic pharmaceutically acceptable edible carriers to make either immediate release or slow release formulations, as is well known in the art. Such edible carriers may be either solid or liquid such as, for example, corn starch, lactose, sucrose, soy flakes, peanut oil, olive oil, sesame oil and propylene glycol. If a  
25 solid carrier is used the dosage form of the compounds may be tablets, capsules, powders, troches or lozenges or top dressing as micro-dispersable forms. If a liquid carrier is used, soft gelatin capsules, or syrup or liquid suspensions, emulsions or solutions may be the dosage form. The dosage forms may also contain adjuvants, such as preserving, stabilizing, wetting or emulsifying agents, solution promoters, etc. They  
30 may also contain other therapeutically valuable substances.

Thus, a significant advantages of the invention include for example, 1) ease of manufacture of the active ingredient loaded biocompatible compositions; 2) versatility



as it relates to the class of polymers and/or active ingredients which may be utilized; 3) higher yields and loading efficiencies; and 4) the provision of sustained release formulations that release active, intact active agents *in vivo*, thus providing for controlled release of an active agent over an extended period of time. In addition,  
5 another advantage is due to the local delivery of the agent with in the digestive tract (*e.g.*, the gizzard) of the organism. As used herein the phrase "contained within" denotes a method for formulating an agent into a composition useful for controlled release, over an extended period of time of the agent.

10 In the sustained-release or slow release compositions of the invention, an effective amount of an agent (*e.g.*, an enzyme or antibiotic) will be utilized. As used herein, sustained release or slow release refers to the gradual release of an agent from a biocompatible material, over an extended period of time. The sustained release can be continuous or discontinuous, linear or non-linear, and this can be accomplished using  
15 one or more biodegradable or non-biodegradable compositions, drug loadings, selection of excipients, or other modifications. However, it is to be recognized that it may be desirable to provide for a "fast" release composition, that provides for rapid release once consumed by the organism. It is also to be understood that by "release" does not necessarily mean that the agent is released from the biocompatible carrier. Rather in  
20 one embodiment, the slow release encompasses slow activation or continual activation of an agent present on the biocompatible composition. For example, a phytase need not be released from the biocompatible composition to be effective. In this embodiment, the phytase is immobilized on the biocompatible composition.

25 The animal feed may be any protein-containing organic meal normally employed to meet the dietary requirements of animals. Many of such protein-containing meals are typically primarily composed of corn, soybean meal or a corn/soybean meal mix. For example, typical commercially available products fed to fowl include Egg  
30 Maker Complete, a poultry feed product of Land O'Lakes AG Services, as well as Country Game & Turkey Grower a product of Agwa, Inc. (see also The Emu Farmer's Handbook by Phillip Minnaar and Maria Minnaar). Both of these commercially available products are typical examples of animal feeds with which the present dietary aid and/or the enzyme phytase may be incorporated to reduce or eliminate the amount

of supplemental phosphorus, zinc, manganese and iron intake required in such compositions.

The present invention is applicable to the diet of numerous animals, which  
5 herein is defined as including mammals (including humans), fowl and fish. In particular, the diet may be employed with commercially significant mammals such as pigs, cattle, sheep, goats, laboratory rodents (rats, mice, hamsters and gerbils), fur-bearing animals such as mink and fox, and zoo animals such as monkeys and apes, as well as domestic mammals such as cats and dogs. Typical commercially significant  
10 avian species include chickens, turkeys, ducks, geese, pheasants, emu, ostrich, loons, kiwi, doves, parrots, cockatiel, cockatoo, canaries, penguins, flamingoes, and quail. Commercially farmed fish such as trout would also benefit from the dietary aids disclosed herein. Other fish that can benefit include, for example, fish (especially in an aquarium or aquaculture environment, *e.g.*, tropical fish), goldfish and other  
15 ornamental carp, catfish, trout, salmon, shark, ray, flounder, sole, tilapia, medaka, guppy, molly, platyfish, swordtail, zebrafish, and loach.

Unless otherwise stated, transformation was performed as described in the method of Sambrook, Fritsch and Maniatus, 1989. The following examples are  
20 intended to illustrate, but not to limit, the invention. While the procedures described in the examples are typical of those that can be used to carry out certain aspects of the invention, other procedures known to those skilled in the art can also be used.

### **EXAMPLE 1**

#### **ISOLATION, BACTERIAL EXPRESSION, AND PURIFICATION OF PHYTASE**

*E.coli* B genomic DNA was obtained from Sigma (Catalog # D-2001), St. Louis, New Jersey.

30 The following primers were used to PCR amplify the gene directly from the genomic DNA:

5' primer      gtttctgaattcaaggaggaatttaaATGAAAGCGATCTTAATCCCATT  
(SEQ ID NO:3); and

3' primer gtttctggatccTTACAAACTGCACGCCGGTAT (SEQ ID NO:4).

Pfu polymerase in the PCR reaction, and amplification was performed according to manufacturers protocol (Stratagene Cloning Systems, Inc., La Jolla, CA).

PCR product was purified and purified product and pQE60 vector (Qiagen) were both digested with EcoRI and BglII restriction endonucleases (New England Biolabs) according to manufacturers protocols. Overnight ligations were performed using standard protocols to yield pQE60.

The amplified sequences were inserted in frame with the sequence encoding for the RBS. The ligation mixture was then used to transform the *E. coli* strain M15/pREP4 (Qiagen, Inc.) by electroporation. M15/pREP4 contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan<sup>r</sup>). Plasmid DNA was isolated and confirmed by restriction analysis. Clones containing the desired constructs were grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture was used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells were grown to an optical density 600 (O.D.<sup>600</sup>) of between 0.4 and 0.6. IPTG ("Isopropyl-B-D-thiogalacto pyranoside") was then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression. Cells were grown an extra 3 to 4 hours. Cells were then harvested by centrifugation.

The primer sequences set out above may also be employed to isolate the target gene from the deposited material by hybridization techniques described above.

Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, within the scope of the appended claims, the invention may be practiced otherwise than as particularly described. It is to be understood that, while the invention has been described with reference to the above detailed description, the foregoing description is intended to illustrate, but not to limit, the scope of the invention. Other aspects, advantages, and modifications of the

invention are within the scope of the following claims. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety.

- 5 This invention also provides for the isolation and use of phytase molecules (nucleic acids and phytase enzymes encoded thereby) from all other strains of *E. coli* (whether virulent or non-virulent, including K12, W, C), as well as all bacteria. These include all known species and strains belonging to:

Thermotogales

- 10 Green Nonsulfur Bacteria

Cyanobacteria & chloroplasts

Low G+C Gram-Positive Bacteria

Fusobacteria

High G+C Gram-Positive Bacteria

- 15 Gytophaga/Flexibacter/Bacteroides group

Fibrobacteria

Spriochaetes

Planctomyces/Chlamydia group

- 20 Purple bacteria (Proteobacteria), including the following subdivisions:

Delta & Epsilon, including:

Desulfuromonas acetoxidans

Desulfosarcina variabilis

Bdellovibrio stolpii

- 25 Nannocystis exedens

Stigmatella aurantiaca

Myxococcus xanthus

Desulfovibrio desulfuricans

Thiovulum sp.

- 30 Campylobacter jejuni

Wolinella succinogenes

Helicobacter pylori

Alpha, including:

Methylobacterium extorquens

- 35 Beijerinckia indica

Hyphomicrobium vulgare

Rhodomicrobium vannielii

Agrobacterium tumefaciens

Brucella abortus

- 40 Rochalimaea quintana

Rhodopseudomonas marina subsp. agilis

Zea mays – mitochondrion

Rickettsia rickettsii

Ehrlichia risticii

- 45 Wolbachia pipientis

Anaplasma marginale

- |    |   |
|----|---|
|    | Erythrobacter longus  |
|    | Rhodospirillum salexigens   |
|    | Rhodobacter capsulatus  |
| 5  | Azospirillum lipoferum  |
|    | Rhodospirillum rubrum   |
|    | Gamma, including:   |
|    | Ectothiorhodospira shaposhnikovii   |
|    | Chromatium vinosum  |
| 10 | Methylobacterium methanica  |
|    | Cardiobacterium hominis   |
|    | Xanthomonas maltophilia   |
|    | Coxiella burnetii   |
|    | Legionella pneumophila subsp. pneumophila   |
| 15 | Oceanospirillum linum   |
|    | Acinetobacter calcoaceticus   |
|    | Pseudomonas aeruginosa  |
|    | Haemophilus influenzae  |
|    | Vibrio parahaemolyticus   |
| 20 | Proteus vulgaris  |
|    | Erwinia carotovora  |
|    | Escherichia coli, including:  |
|    | Beta, including:  |
| 25 | Eikenella corrodens   |
|    | Neisseria gonorrhoeae   |
|    | Vitreoscilla stercoraria  |
|    | Chromobacterium violaceum   |
|    | Alcaligenes faecalis  |
| 30 | Rubrivivax gelatinosus  |
|    | Pseudomonas testosteroni  |
|    | Nitrosomonas europae  |
|    | Spirillum volutans  |
| 35 | Such phytase molecules can be isolated from these bacteria by known methods, including library screening methods, <i>e.g.</i> expression screening, hybridization methods, PCR ( <i>e.g.</i> see Sambrook, 1989). |

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- 25

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What is claimed is:

1. A method for improving the nutritional value of a phytate-containing foodstuff comprising:

5 contacting said phytate-containing foodstuff with a substantially pure phytase enzyme having an amino acid sequence selected from the group consisting of SEQ ID NO:2, such that said substantially pure phytase enzyme catalyzes the liberation of inorganic phosphate from the phytate in said phytate-containing foodstuff.

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2. The method of claim 1, wherein said substantially pure phytase enzyme is produced by a recombinant expression system comprising a phytase-encoding nucleic acid having a nucleotide sequence selected from the group consisting of:

a) SEQ ID NO:1, and

15

b) SEQ ID NO:1 wherein T can also be U;

wherein the expression of the phytase-encoding nucleic acid leads to the production of said substantially pure phytase enzyme.

3. The method of claim 1, wherein the liberation of the inorganic phosphate from the phytate in said phytate-containing foodstuff occurs prior to the ingestion of said phytate-containing foodstuff by a recipient organism.

20

4. The method of claim 1, wherein the liberation of the inorganic phosphate from the phytate in said phytate-containing foodstuff occurs after the ingestion of said phytate-containing foodstuff by a recipient organism.

25

5. The method of claim 1, wherein the liberation of the inorganic phosphate from the phytate in said phytate-containing foodstuff occurs in part prior to and in part after the ingestion of said phytate-containing foodstuff by a recipient organism.

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6. A recombinant expression system for use in the method of claim 2, wherein said recombinant expression system is contained in a host cell and expresses a

nucleotide sequence encoding a phytase enzyme having an amino acid sequence as set forth in SEQ ID NO:2, and wherein the nucleotide sequence encoding said enzyme is operably linked to a transcription control sequence operable in said host cell.

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7. A vector which comprises the expression system according to claim 6.

8. The expression system of claim 6, wherein the control sequence comprises a constitutive promoter.

10

9. The expression system of claim 6, wherein the control sequence comprises a tissue-specific promoter.

10. The expression system of claim 6, wherein said host cell is a prokaryotic cell.

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11. The expression system of claim 6, wherein said host cell is a eukaryotic cell.

12. The expression system of claim 6, wherein said host cell is a plant cell.

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13. The expression system of claim 6, wherein said nucleotide sequence is preceded by a polynucleotide sequence encoding a signal peptide operably linked to said nucleotide sequence.

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14. The expression system of claim 13, wherein said signal peptide is the PR protein PR-S signal peptide from tobacco.

15. A prokaryotic cell modified to contain the expression system of claim 6.

16. A eukaryotic cell modified to contain the expression system of claim 6.

30

17. A plant cell, plant part or plant modified to contain the expression system of claim 6.

18. A method to produce an animal feed containing a microbial phytase comprising:
- a) culturing the plant cell, plant part or plant of claim 17 under conditions wherein said nucleotide sequence is expressed; and
  - b) converting said plant cells, plant parts or plants into a composition
- 5 suitable for animal feed.

19. A feed composition for animals which comprises the plant seeds, plant cells, plant parts or plants of claim 17 in admixture with a phytate-containing foodstuff.

20. A method to treat a human or an animal able to benefit from digestive enhancement by the activity of an exogenous phytase enzyme, which method comprises administering to said human or animal an amount of plant seeds, plant cells, plant parts or plants of a transgenic plant, wherein said transgenic plant is modified to contain an expression system which expresses a nucleotide sequence encoding a phytase enzyme in an amount effective to provide phytase activity in said human's or animal's digestive tract.

21. A transgenic non-human organism whose genome comprises a heterologous nucleic acid sequence encoding a polypeptide having phytase activity, wherein said transgene results in expression of a phytase polypeptide.

22. A method of generating a variant comprising:

obtaining a nucleic acid comprising a sequence as set forth in SEQ ID NO: 1, sequences substantially identical thereto, sequences complementary thereto, fragments comprising at least 30 consecutive nucleotides thereof, and fragments comprising at least 30 consecutive nucleotides of the sequences complementary to SEQ ID NO:1; and

modifying one or more nucleotides in said sequence to another nucleotide, deleting one or more nucleotides in said sequence, or adding one or more nucleotides to said sequence.



23. The method of claim 22, wherein the modifications are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, ligation reassembly, GSSM and any combination thereof.
24. The method of claim 22, wherein the modifications are introduced by error-prone PCR.
25. The method of claim 22, wherein the modifications are introduced by shuffling.
26. The method of claim 22, wherein the modifications are introduced by oligonucleotide-directed mutagenesis.
27. The method of claim 22, wherein the modifications are introduced by assembly PCR.
28. The method of claim 22, wherein the modifications are introduced by sexual PCR mutagenesis.
29. The method of claim 22, wherein the modifications are introduced by *in vivo* mutagenesis.
30. The method of claim 22, wherein the modifications are introduced by cassette mutagenesis.
31. The method of claim 22, wherein the modifications are introduced by recursive ensemble mutagenesis.

32. The method of claim 22, wherein the modifications are introduced by exponential ensemble mutagenesis.

33. The method of claim 22, wherein the modifications are introduced by site-specific mutagenesis.

34. A computer readable medium having stored thereon a nucleic acid sequence as set forth in SEQ ID NO:1, and sequences substantially identical thereto, or a polypeptide sequence as set forth in SEQ ID NO:2, and sequences substantially identical thereto.

35. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a nucleic acid sequence as set forth in SEQ ID NO:1, and sequences substantially identical thereto, or a polypeptide sequence as set forth in SEQ ID NO:2 and sequences substantially identical thereto.

36. The computer system of claim 35, further comprising a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon.

37. The computer system of claim 36, wherein the sequence comparison algorithm comprises a computer program which indicates polymorphisms.

38. The computer system of claim 35, further comprising an identifier which identifies features in said sequence.

39. A method for comparing a first sequence to a reference sequence or a database of sequences wherein said first sequence is a nucleic acid sequence as set forth in SEQ ID NO:1, and sequences substantially identical thereto, or a polypeptide sequence as set forth in SEQ ID NO:2, and sequences substantially identical thereto comprising:

reading the first sequence and the reference sequence or database of sequences through use of a computer program which compares sequences; and



## **ABSTRACT**


A purified recombinant phytase enzyme derived from *Escherichia coli* B. The enzyme has a molecular weight of about 47.1 kilodaltons and has phytase activity. The enzyme can be produced from native or recombinant host cells and can be used to aid in the digestion of phytate where desired. In particular, the phytase of the present invention can be used in foodstuffs to improve the feeding value of phytate rich ingredients.

10

FIGURE 1A

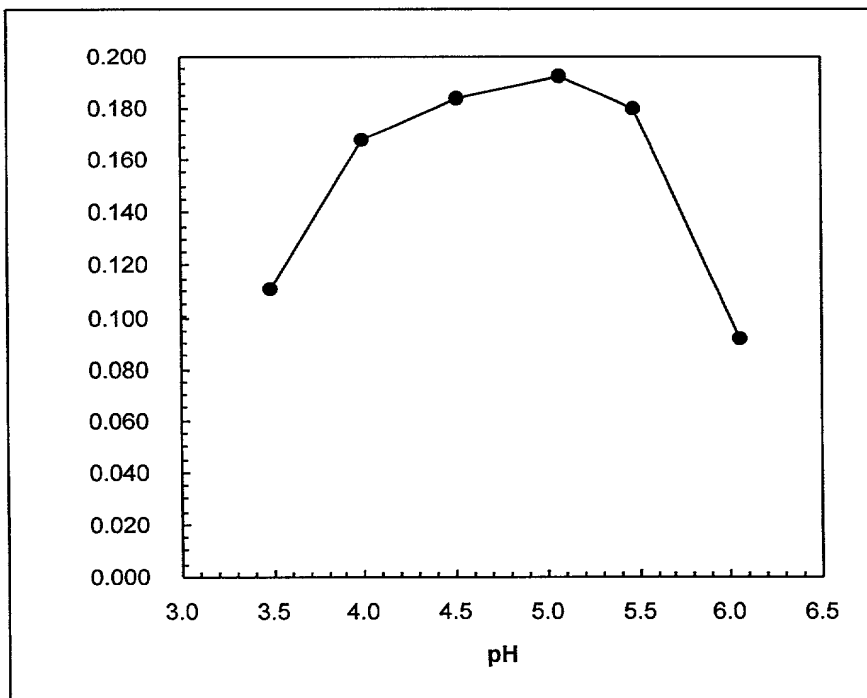
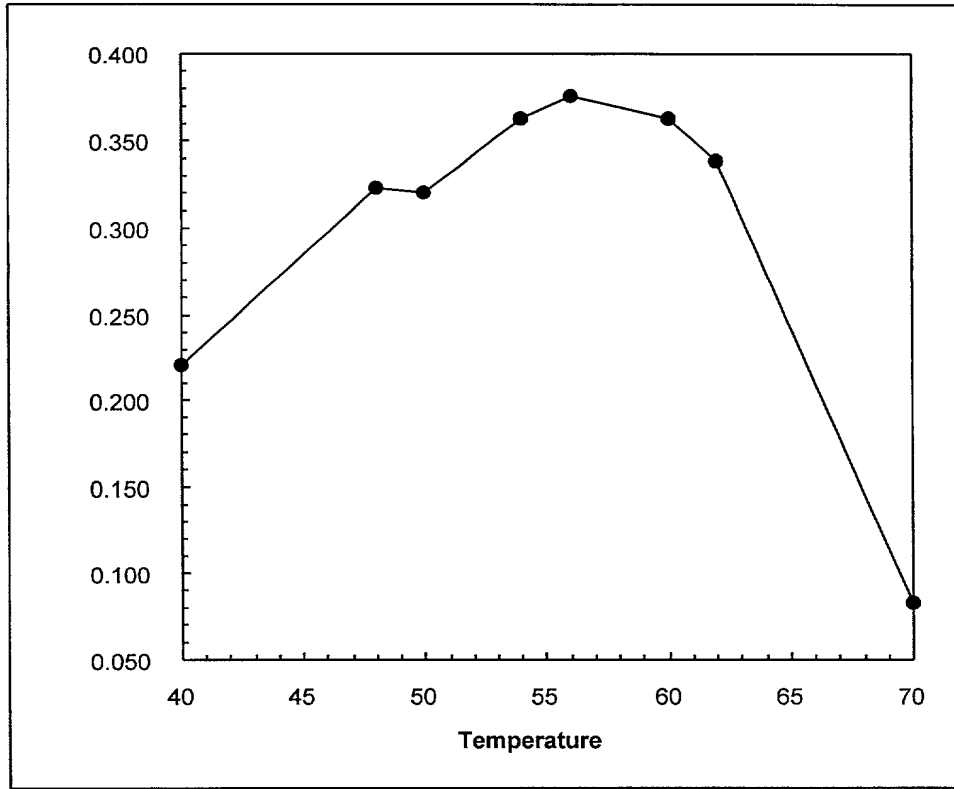
(SEQ ID NO:1-nucleotide sequence and SEQ ID NO:2-amino acid sequence)  
*Escherichia coli* B Phytase Sequence

1  
ATG AAA GCG ATC TTA ATC CCA TTT TTA TCT CTT CTG ATT CCG TTA ACC CCG  
Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr Pro  
  
CAA TCT GCA TTC GCT CAG AGT GAG CCG GAG CTG AAG CTG GAA AGT GTG GTG  
Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser Val Val  
  
ATT GTC AGT CGT CAT GGT GTG CGT GCT CCA ACC AAG GCC ACG CAA CTG ATG  
Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr Gln Leu Met  
  
CAG GAT GTC ACC CCA GAC GCA TGG CCA ACC TGG CCG GTA AAA CTG GGT TGG  
Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val Lys Leu Gly Trp  
  
CTG ACA CCG CGN GGT GGT GAG CTA ATC GCC TAT CTC GGA CAT TAC CAA CGC  
Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu Gly His Tyr Gln Arg  
  
CAG CGT CTG GTA GCC GAC GGA TTG CTG GCG AAA AAG GGC TGC CCG CAG TCT  
Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys Lys Gly Cys Pro Gln Ser  
  
GGT CAG GTC GCG ATT ATT GCT GAT GTC GAC GAG CGT ACC CGT AAA ACA GGC  
Gly Gln Val Ala Ile Ile Ala Asp Val Asp Glu Arg Thr Arg Lys Thr Gly  
  
GAA GCC TTC GCC GCC GGG CTG GCA CCT GAC TGT GCA ATA ACC GTA CAT ACC  
Glu Ala Phe Ala Ala Gly Leu Ala Pro Asp Cys Ala Ile Thr Val His Thr  
  
CAG GCA GAT ACG TCC AGT CCC GAT CCG TTA TTT AAT CCT CTA AAA ACT GGC  
Gln Ala Asp Thr Ser Ser Pro Asp Pro Leu Phe Asn Pro Leu Lys Thr Gly  
  
GTT TGC CAA CTG GAT AAC GCG AAC GTG ACT GAC GCG ATC CTC AGC AGG GCA  
Val Cys Gln Leu Asp Asn Ala Asn Val Thr Asp Ala Ile Leu Ser Arg Ala  
  
GGA GGG TCA ATT GCT GAC TTT ACC GGG CAT CGG CAA ACG GCG TTT CGC GAA  
Gly Gly Ser Ile Ala Asp Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu  
  
CTG GAA CGG GTG CTT AAT TTT CCG CAA TCA AAC TTG TGC CTT AAA CGT GAG  
Leu Glu Arg Val Leu Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu  
  
AAA CAG GAC GAA AGC TGT TCA TTA ACG CAG GCA TTA CCA TCG GAA CTC AAG  
Lys Gln Asp Glu Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys  
  
GTG AGC GCC GAC AAT GTC TCA TTA ACC GGT GCG GTA AGC CTC GCA TCA ATG  
Val Ser Ala Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met  
  
CTG ACG GAG ATA TTT CTC CTG CAA CAA GCA CAG GGA ATG CCG GAG CCG GGG  
Leu Thr Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly  
  
TGG GGA AGG ATC ACC GAT TCA CAC CAG TGG AAC ACC TTG CTA AGT TTG CAT  
Trp Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His  
  
AAC GCG CAA TTT TAT TTG CTA CAA CGC ACG CCA GAG GTT GCC CGC AGC CGC

1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2

**FIGURE 2**  
**pH/Temperature Profile and Stability**



## DECLARATION FOR PATENT APPLICATION

As a below-named inventor, I hereby declare that:

My residence, post office address and citizenship is as stated below next to my name.

I believe that I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF, the specification of which

\_\_\_\_\_ is attached hereto.

  X   was filed on May 25, 2000 as U.S. Application Serial No. \_\_\_\_\_  
(the "Application") (Docket No. DIVER1370-4).

I hereby authorize and request insertion of the application serial number of the Application when officially known.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose to the United States Patent and Trademark Office all information known to me to be material to patentability of the subject matter of the Application as defined in Title 37, Code of Federal Regulations ("C.F.R."), § 1.56.

With respect to the Application, I hereby claim the benefit under 35 U.S.C. Section 119(e) of any United States provisional application(s) listed below:

\_\_\_\_\_  
(Application Serial No.)      (Filing Date)

With respect to the Application, I hereby claim the benefit under 35 U.S.C. Section 120 of any United States application(s), or Section 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of the application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. Section 112, I acknowledge the duty to disclose to the United States Patent and Trademark Office all information known to me to be material to patentability of the subject matter of the



Application as defined in Title 37, C.F.R., Section 1.56 which became available between the filing date of the prior application and the national or PCT International filing date of the Application:

|   |   |   |
|---|---|---|
| <u>09/318,528</u><br>(Application Serial No.) | <u>May 25, 1999</u><br>(Filing Date)    | <u>Pending</u><br>(Status)<br>(patented, pending, abandoned)            |
| <u>09/291,931</u><br>(Application Serial No.) | <u>April 13, 1999</u><br>(Filing Date)  | <u>Pending</u><br>(Status)<br>(patented, pending, abandoned)            |
| <u>09/259,214</u><br>(Application Serial No.) | <u>March 1, 1999</u><br>(Filing Date)   | <u>Pending</u><br>(Status)<br>(patented, pending, abandoned)            |
| <u>08/910,798</u><br>(Application Serial No.) | <u>August 13, 1997</u><br>(Filing Date) | <u>Issued (5,876,997)</u><br>(Status)<br>(patented, pending, abandoned) |

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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Inventor's signature: \_\_\_\_\_

Date: \_\_\_\_\_

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Thereof

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<210> 1

<211> 1323

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<400> 1

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| atg | aaa | gcg | atc | tta | atc | cca | ttt | tta | tct | ctt | ctg | att | ccg | tta | acc | 48 |
| Met | Lys | Ala | Ile | Leu | Ile | Pro | Phe | Leu | Ser | Leu | Leu | Ile | Pro | Leu | Thr |    |
| 1   |     |     | 5   |     |     |     |     |     | 10  |     |     |     |     | 15  |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| ccg | caa | tct | gca | ttc | gct | cag | agt | gag | ccg | gag | ctg | aag | ctg | gaa | agt | 96 |
| Pro | Gln | Ser | Ala | Phe | Ala | Gln | Ser | Glu | Pro | Glu | Leu | Lys | Leu | Glu | Ser |    |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |    |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gtg | gtg | att | gtc | agt | cgt | cat | ggc | gtg | cgt | gct | cca | acc | aag | gcc | acg | 144 |
| Val | Val | Ile | Val | Ser | Arg | His | Gly | Val | Arg | Ala | Pro | Thr | Lys | Ala | Thr |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |

|   |     |
|---|-----|
| caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg ccg gta | 192 |
| Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val |     |
| 50 55 60  |     |
| aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc tat ctc | 240 |
| Lys Leu Gly Trp Leu Thr Pro Xaa Gly Gly Glu Leu Ile Ala Tyr Leu |     |
| 65 70 75 80   |     |
| gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg gcg aaa | 288 |
| Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys |     |
| 85 90 95  |     |
| aag ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat gtc gac | 336 |
| Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp |     |
| 100 105 110   |     |
| gag cgt acc cgt aaa aca ggc gaa gcc ttc gcc gcc ggg ctg gca cct | 384 |
| Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro |     |
| 115 120 125   |     |
| gac tgt gca ata acc gta cat acc cag gca gat acg tcc agt ccc gat | 432 |
| Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp |     |
| 130 135 140   |     |
| ccg tta ttt aat cct cta aaa act ggc gtt tgc caa ctg gat aac gcg | 480 |
| Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala |     |
| 145 150 155 160   |     |
| aac gtg act gac gcg atc ctc agc agg gca gga ggg tca att gct gac | 528 |
| Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp |     |
| 165 170 175   |     |
| ttt acc ggg cat cgg caa acg gcg ttt cgc gaa ctg gaa cgg gtg ctt | 576 |
| Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu |     |
| 180 185 190   |     |
| aat ttt ccg caa tca aac ttg tgc ctt aaa cgt gag aaa cag gac gaa | 624 |
| Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu |     |
| 195 200 205   |     |
| agc tgt tca tta acg cag gca tta cca tcg gaa ctc aag gtg agc gcc | 672 |
| Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala |     |
| 210 215 220   |     |
| gac aat gtc tca tta acc ggt gcg gta agc ctc gca tca atg ctg acg | 720 |
| Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr |     |
| 225 230 235 240   |     |
| gag ata ttt ctc ctg caa caa gca cag gga atg ccg gag ccg ggg tgg | 768 |
| Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp |     |
| 245 250 255   |     |

|   |      |
|---|------|
| gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt ttg cat | 816  |
| Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His |      |
| 260 265 270   |      |
| aac gcg caa ttt tat ttg cta caa cgc acg cca gag gtt gcc cgc agc | 864  |
| Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser |      |
| 275 280 285   |      |
| cgc gcc acc ccg tta ttg gat ttg atc atg gca gcg ttg acg ccc cat | 912  |
| Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His |      |
| 290 295 300   |      |
| cca ccg caa aaa cag gcg tat ggt gtg aca tta ccc act tca gta ctg | 960  |
| Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu |      |
| 305 310 315 320   |      |
| ttt att gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg | 1008 |
| Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu |      |
| 325 330 335   |      |
| gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg cca ggt | 1056 |
| Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly |      |
| 340 345 350   |      |
| ggt gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac agc cag | 1104 |
| Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln |      |
| 355 360 365   |      |
| tgg att cag gtt tcg ctg gtc ttc cag act tta cag cag atg cgt gat | 1152 |
| Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp |      |
| 370 375 380   |      |
| aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc | 1200 |
| Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr |      |
| 385 390 395 400   |      |
| ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg ttg gca | 1248 |
| Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala |      |
| 405 410 415   |      |
| ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc agt ttg | 1296 |
| Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu |      |
| 420 425 430   |      |
| aga tct cat cac cat cac cat cac taa                             | 1323 |
| Arg Ser His His His His His His                                 |      |
| 435 440   |      |

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 <213> Escherichia coli

<400> 2

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ala | Ile | Leu | Ile | Pro | Phe | Leu | Ser | Leu | Leu | Ile | Pro | Leu | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Gln | Ser | Ala | Phe | Ala | Gln | Ser | Glu | Pro | Glu | Leu | Lys | Leu | Glu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Val | Ile | Val | Ser | Arg | His | Gly | Val | Arg | Ala | Pro | Thr | Lys | Ala | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Leu | Met | Gln | Asp | Val | Thr | Pro | Asp | Ala | Trp | Pro | Thr | Trp | Pro | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Lys | Leu | Gly | Trp | Leu | Thr | Pro | Xaa | Gly | Gly | Glu | Leu | Ile | Ala | Tyr | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | His | Tyr | Gln | Arg | Gln | Arg | Leu | Val | Ala | Asp | Gly | Leu | Leu | Ala | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Gly | Cys | Pro | Gln | Ser | Gly | Gln | Val | Ala | Ile | Ile | Ala | Asp | Val | Asp |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Arg | Thr | Arg | Lys | Thr | Gly | Glu | Ala | Phe | Ala | Ala | Gly | Leu | Ala | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Cys | Ala | Ile | Thr | Val | His | Thr | Gln | Ala | Asp | Thr | Ser | Ser | Pro | Asp |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Leu | Phe | Asn | Pro | Leu | Lys | Thr | Gly | Val | Cys | Gln | Leu | Asp | Asn | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Asn | Val | Thr | Asp | Ala | Ile | Leu | Ser | Arg | Ala | Gly | Gly | Ser | Ile | Ala | Asp |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |
| Phe | Thr | Gly | His | Arg | Gln | Thr | Ala | Phe | Arg | Glu | Leu | Glu | Arg | Val | Leu |
|     |     | 180 |     |     |     |     | 185 |     |     |     |     |     | 190 |     |     |
| Asn | Phe | Pro | Gln | Ser | Asn | Leu | Cys | Leu | Lys | Arg | Glu | Lys | Gln | Asp | Glu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Ser | Cys | Ser | Leu | Thr | Gln | Ala | Leu | Pro | Ser | Glu | Leu | Lys | Val | Ser | Ala |
|     | 210 |     |     |     | 215 |     |     |     |     |     | 220 |     |     |     |     |
| Asp | Asn | Val | Ser | Leu | Thr | Gly | Ala | Val | Ser | Leu | Ala | Ser | Met | Leu | Thr |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Glu | Ile | Phe | Leu | Leu | Gln | Gln | Ala | Gln | Gly | Met | Pro | Glu | Pro | Gly | Trp |
|     |     |     | 245 |     |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gly | Arg | Ile | Thr | Asp | Ser | His | Gln | Trp | Asn | Thr | Leu | Leu | Ser | Leu | His |
|     |     | 260 |     |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Asn | Ala | Gln | Phe | Tyr | Leu | Leu | Gln | Arg | Thr | Pro | Glu | Val | Ala | Arg | Ser |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Arg | Ala | Thr | Pro | Leu | Leu | Asp | Leu | Ile | Met | Ala | Ala | Leu | Thr | Pro | His |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Pro | Pro | Gln | Lys | Gln | Ala | Tyr | Gly | Val | Thr | Leu | Pro | Thr | Ser | Val | Leu |
| 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |     | 320 |
| Phe | Ile | Ala | Gly | His | Asp | Thr | Asn | Leu | Ala | Asn | Leu | Gly | Gly | Ala | Leu |
|     |     |     | 325 |     |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Glu | Leu | Asn | Trp | Thr | Leu | Pro | Gly | Gln | Pro | Asp | Asn | Thr | Pro | Pro | Gly |
|     |     | 340 |     |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gly | Glu | Leu | Val | Phe | Glu | Arg | Trp | Arg | Arg | Leu | Ser | Asp | Asn | Ser | Gln |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ile | Gln | Val | Ser | Leu | Val | Phe | Gln | Thr | Leu | Gln | Gln | Met | Arg | Asp |
| 370 |     |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Lys | Thr | Pro | Leu | Ser | Leu | Asn | Thr | Pro | Pro | Gly | Glu | Val | Lys | Leu | Thr |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Leu | Ala | Gly | Cys | Glu | Glu | Arg | Asn | Ala | Gln | Gly | Met | Cys | Ser | Leu | Ala |
|     |     |     | 405 |     |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Gly | Phe | Thr | Gln | Ile | Val | Asn | Glu | Ala | Arg | Ile | Pro | Ala | Cys | Ser | Leu |
|     |     |     | 420 |     |     |     | 425 |     |     |     |     |     | 430 |     |     |
| Arg | Ser | His | His | His | His | His | His |     |     |     |     |     |     |     |     |
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33



ATTORNEY DOCKET NO. DIVER1370-4

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Applicant: Jay M. Short et al. Art Unit: Unassigned  
Serial No.: Unassigned Examiner: Unassigned  
Filed: Herewith  
Parent Serial No.: 09/318,528  
Parent Filing Date: May 25, 1999  
Title: RECOMBINANT BACTERIAL PHYTASES AND USES THEREOF

Box Patent Application  
Assistant Commissioner of Patents  
Washington, D.C. 20231

|  |
|--|
| <p>"EXPRESS MAIL" Mailing Label Number: <b>EL476993090US</b><br/>Date of Deposit <b>May 25, 2000</b><br/>I hereby certify under 37 CFR 1.10 that this correspondence is being deposited with the United States Postal Service as "Express Mail Post Office to Addressee" with sufficient postage on the date indicated above and is addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231<br/><br/>_____<br/>MIKHAIL BAYLEY<br/><br/>_____<br/><i>Mikhail Bayley</i></p> |
|--|

**PERMISSION TO USE SEQUENCE LISTING**

Sir:

The above-identified patent application lacks a substitute paper copy of the Sequence Listing for inclusion into the Specification, as well as a computer readable form of the Sequence Listing. Applicants respectfully direct the attention of the Office to the following:

1. A complete paper copy of the Sequence Listing is to be inserted following the Abstract on page 129 and before the Drawings. Please insert the Sequence Listing beginning with page 1 and numbering consecutively thereafter. A paper copy of the Sequence Listing is included herewith, and is identical to the computer readable copy of the Sequence Listing filed in U.S. Patent Application Number 09/318,528 (the "528 application"), filed May 25, 1999.



2. A computer-readable form in this application is identical with that filed in '528 application, filed October 15, 1999. Pursuant to 37 CFR §1.821(e), please use the last-filed computer-readable form filed in the '528 application as the computer-readable form for application filed herewith. It is understood that the Patent and Trademark Office will make the necessary change in application number and filing date for the computer readable form that will be used for application filed herewith.

I hereby state, as required by 37 C.F.R. § 1.821(g), that the enclosed submission includes no new matter. Applicants submit that the foregoing satisfies the requirements of Rule §1.821. If there are any questions regarding this response, the Office is invited to contact the undersigned.

No fee is deemed necessary in connection with the filing of this paper. However, if any fee is required, the Commissioner is hereby authorized to charge the amount of this fee, or credit any overpayments, to Deposit Account No. 50-1355.

Respectfully submitted,

Date:

5/25/00



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Registration No. 38,347

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San Diego, California 92121-2189